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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07K 14/00	A2	(11) International Publication Number: WO 98/55508 (43) International Publication Date: 10 December 1998 (10.12.98)
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(54) Title: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs ENCODING THESE PROTEINS (57) Abstract Proteins comprising any of the amino acid sequences of SEQ ID NOS: 1 to 18 and DNAs encoding said proteins and comprising any of the nucelotide sequences of SEQ ID NOS: 19 to 36 are provided.		

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DESCRIPTION

Human Proteins Having Transmembrane
Domains and DNAs Encoding These Proteins

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FIELD OF THE INVENTION

The present invention relates to human proteins having transmembrane domains and cDNAs encoding these proteins. The membrane proteins of this invention can be used as pharmaceuticals or as antigens for preparing antibodies against said proteins. The cDNAs of the invention can be used as probes for the gene diagnosis and gene sources for the gene therapy. The cDNAs can also be used as gene sources for large-scale production of the membrane proteins encoded by the same. The cells into which the genes encoding the membrane proteins are introduced for expression of such membrane proteins in large amounts can be used for detection of the corresponding ligands, screening of low molecular weight medicines, etc.

20 BACKGROUND OF THE INVENTION

Membrane proteins play important roles as signal receptors, ion channels, transporters, etc. for the material transportation or information transmission mediated by the cell membrane. For instance, they are known to serve as receptors for various cytokines, ion channels for sodium ion, potassium ion, chloride ion, etc., transporters for saccharides and amino acids, and so on. The genes for many of them have been cloned already.

In recent years, it was clarified that the abnormalities

of these membrane proteins are related to a number of hitherto cryptogenic diseases. For example, a gene for a membrane protein having 12 transmembrane domains was identified as the gene responsible for cystic fibrosis [Rommens, J. M. et al.,
5 Science 245: 1059-1065 (1989)]. It was also clarified that several membrane proteins act as the receptors when a virus infects the cells. For example, HIV-1 was revealed to infect into the cells through the mediation of a membrane protein fusin, a membrane protein on the T-cell membrane, having a CD-4
10 antigen and 7 transmembrane domains [Feng, Y. et al., Science 272: 872-877 (1996)]. Therefore, the discovery of new membrane proteins is anticipated to lead to the elucidation of the causes of many diseases, and the isolation of new genes coding for the membrane proteins is desired.

15 Heretofore, owing to the difficulty in their purification, many of membrane proteins have been isolated by an approach from the gene side. A general method is the so-called expression cloning which comprises transfection of a cDNA library in the animal cells to express the cDNA and detection
20 of the cells expressing the target membrane protein on the membrane by an immunological technique using an antibody or a physiological technique for the change in the membrane permeability. However, this method is applicable only to cloning of a gene for a membrane protein with a known function.

25 In general, membrane proteins possess hydrophobic transmembrane domains inside the proteins which are synthesized in the ribosome. Said domains remain in the phospholipid to be trapped in the membrane. Accordingly, the evidence of the cDNA for encoding the membrane protein is provided by determination

of the whole base sequence of a full-length cDNA and detection of highly hydrophobic transmembrane domains in the amino acid sequence of the protein encoded by said cDNA.

As a result of the extensive study, there have successfully been obtained human proteins having transmembrane domains, particularly comprising any of the amino acid sequences of SEQ ID NOS: 1 to 18, by cloning cDNAs coding for proteins having transmembrane domains, particularly comprising any of the nucleotide sequences of SEQ ID NOS: 19 to 36, from a human full-length cDNA bank. The present invention is based on the above success.

SUMMARY OF THE INVENTION

A main object of the present invention is to provide novel human proteins having transmembrane domains, particularly comprising any of the amino acid sequences of SEQ ID NOS: 1 to 18. Another object of this invention is to provide DNAs coding for said novel proteins, particularly comprising any of the nucleotide sequences of SEQ ID NOS: 19 to 36. A further object of the invention is to provide expression vectors capable of in vitro translating said DNAs or expressing said DNAs in eukaryotic cells. A still further object of the invention is to provide transformed eukaryotic cells capable of expressing said DNAs to produce said proteins.

In one embodiment, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of the amino acid sequences of SEQ ID NOS: 1 to 18 and their fragments.

In another embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of the nucleotide sequences of SEQ ID NOS: 19 to 36.

- 5 In a further embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of the nucleotide sequences of SEQ ID NOS: 37 to 54.

10 BRIEF DESCRIPTION OF DRAWINGS

Figure 1: A figure depicting the structure of the secretory signal sequence detection vector pSSD3.

Figure 2: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01263.

- 15 Figure 3: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01299.

Figure 4: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01347.

- 20 Figure 5: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01440.

Figure 6: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01526.

Figure 7: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10230.

- 25 Figure 8: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10389.

Figure 9: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10408.

Figure 10: A figure depicting the hydrophobicity/hydro-

philicity profile of the protein encoded by clone HP10412.

Figure 11: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10413.

Figure 12: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10415.

Figure 13: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10419.

Figure 14: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10424.

10 Figure 15: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10428.

Figure 16: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10429.

15 Figure 17: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10432.

Figure 18: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10433.

Figure 19: A figure depicting the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10480.

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BEST MODE FOR CARRING OUT INVENTION

The proteins of the present invention can be obtained, for example, by isolation from human organs, cell lines, etc., by chemical synthesis on the basis of the amino acid sequences as
25 herein disclosed, or by recombinant DNA technology using the DNA encoding the transmembrane domains of the invention. Among them, adoption of the recombinant DNA technology is preferred. Specifically, each of the proteins may be prepared by in vitro transcription of a vector comprising the cDNA of the invention

to make RNA and in vitro translation using this RNA as a template to accomplish in vitro expression. Also, each of the proteins may be prepared in a large amount by the use of *Escherichia coli*, *Bacillus subtilis*, yeasts, animal cells, etc.

5 comprising a suitable expression vector having the DNA encoding such protein.

In the case of producing the protein of the invention by the use of a microorganism such as *Escherichia coli*, the translation region of the cDNA of the invention is constructed
10 in an expression vector having an origin, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator, etc. that can be replicated in the microorganism and, after transformation of the host cells with said expression vector, the resultant transformant is incubated, whereby the protein
15 encoded by said cDNA can be produced in a large amount in the microorganism. In that case, a protein fragment containing an optional region can be obtained by performing the expression with inserting an initiation codon and a termination codon before and after the optional translation region. Alternatively,
20 ly, a fusion protein with another protein can be expressed. Only a protein portion encoding said cDNA can be obtained by cleavage of said fusion protein with an appropriate protease.

For production of the protein of the invention by expression of DNA coding for such protein in eukaryotic cells,
25 the translation region of said cDNA may be recombined into an expression vector for eukaryotic cells having a promoter, a splicing domain, a poly(A) addition site, etc., followed by introduction into eukaryotic cells so that the protein of the invention is produced as a membrane protein on the cell

membrane surface. Examples of the expression vector are pKA1, pED6_dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vector, pRS, pYES2, etc. As the eukaryotic cells, there are exemplified mammalian animal culture cells (e.g. simian kidney
5 cells COS7, chinese hamster ovary cells CHO), budding yeasts, Schizosaccharomyces pombe, silkworm cells, Xenopus laevis egg cells, etc., but any other eukaryotic cells may also be used insofar as the protein of the invention can be expressed on the membrane surface. In order to introduce the expression vector
10 into eukaryotic cells, there may be adopted any conventional procedure such as electroporation, calcium phosphate method, liposome method or DEAE dextran method.

The proteins of the present invention include peptide fragments (5 or more amino acid residues) containing any
15 partial amino acid sequence of the amino acid sequences of SEQ ID NOS: 1 to 18. These fragments can be used as antigens for preparation of the antibodies. Also, the proteins of the invention that have signal sequences appear in the form of maturation proteins on the cell surface, after the signal
20 sequences are removed. Therefore, these maturation proteins shall come within the scope of the present invention. The N-terminal amino acid sequences of the maturation proteins can be easily identified by using the method for the cleavage-site determination in a signal sequence [Japan Patent Kokai No.
25 187100/96]. Further, many membrane proteins are subjected to the processing on the cell surface to be converted to the secretor forms. These secretor proteins or peptides shall come within the scope of the present invention. When glycosylation sites are present in the amino acid sequences, expression in

appropriate animal cells affords glycosylated proteins. Therefore, these glycosylated proteins or peptides also shall come within the scope of the invention.

The DNAs of the invention include all DNAs encoding the
5 above-mentioned proteins. Said DNAs can be obtained using the method by chemical synthesis, the method by cDNA cloning, and so on.

Each of the cDNAs of the invention can be cloned from, for example, the cDNA libraries of the human cell origin. The cDNA
10 is synthesized using as a template a poly(A)⁺ RNA extracted from human cells. The human cells may be cells delivered from the human body, for example, by the operation or may be the culture cells. The cDNA can be synthesized by using any method selected from the Okayama-Berg method [Okayama, H. and Berg,
15 P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and Hoffman, J. Gene 25: 263-269 (1983)], and so on, but it is preferred to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)] as illustrated in Examples in order to obtain a full-length clone in an effective manner.

20 The primary selection of a cDNA encoding a human protein having transmembrane domains is performed by the sequencing of a partial base sequence of the cDNA clone selected at random from the cDNA libraries, sequencing of the amino acid sequence encoded by the base sequence, and recognition of the presence
25 or absence of hydrophobic site(s) in the resulting N-terminal amino acid sequence region. Next, the secondary selection is carried out by determination of the whole base sequence by the sequencing and the protein expression by the in vitro translation. The ascertainment of the cDNA of the present

invention for encoding the protein having the secretory signal sequence is performed by using the signal sequence detection method [Yokoyama-Kobayashi, M. et al., Gene 163: 193-196 (1995)]. In other words, the ascertainment for the coding
5 portion of the inserted cDNA fragment to function as a signal sequence is provided by fusing a cDNA fragment encoding the N-terminus of the target protein with a cDNA encoding the protease domain of urokinase and then expressing the resulting cDNA in COS7 cells to detect the urokinase activity in the cell
10 culture medium. On the other hand, the N-terminal region is judged to remain in the membrane in the case where the urokinase activity is not detected in the cell culture medium.

The cDNAs of the invention are characterized by containing any of the nucleotide sequences of SEQ ID NOS: 19 to 36 or any
15 of the nucleotide sequences of SEQ ID NOS: 37 to 54. Table 1 summarizes the clone number (HP number), the cells affording the cDNA, the total nucleotide number of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

5	Sequence Number	HP Number	Cells	Number of Nucleotides	Number of Amino Acid Residues
10	1, 19, 37	HP01263	Liver	1502	382
	2, 20, 38	HP01299	Liver	1349	317
	3, 21, 39	HP01347	Liver	1643	296
15	4, 22, 40	HP01440	Stomach cancer	729	197
	5, 23, 41	HP01526	Stomach cancer	1322	221
20	6, 24, 42	HP10230	Stomach cancer	3045	251
	7, 25, 43	HP10389	KB	653	106
	8, 26, 44	HP10408	Stomach cancer	439	78
25	9, 27, 45	HP10412	Stomach cancer	1131	314
	10, 28, 46	HP10413	Stomach cancer	1875	195
30	11, 29, 47	HP10415	Stomach cancer	1563	462
	12, 30, 48	HP10419	Stomach cancer	2030	247
	13, 31, 49	HP10424	Stomach cancer	493	113
35	14, 32, 50	HP10428	KB	2044	365
	15, 33, 51	HP10429	Stomach cancer	1043	226
40	16, 34, 52	HP10432	Liver	972	129
	17, 35, 53	HP10433	Liver	695	163
45	18, 36, 54	HP10480	Stomach cancer	1914	193

Hereupon, the same clone as any of the cDNAs of the invention can be easily obtained by screening of the cDNA libraries constructed from the cell line or the human tissues employed in the invention, by the use of an oligonucleotide probe synthesized on the basis of the corresponding cDNA nucleotide sequence of SEQ ID NOS: 37 to 54.

In general, the polymorphism due to the individual difference is frequently observed in human genes. Therefore, any cDNA that is subjected to insertion or deletion of one or plural nucleotides and/or substitution with other nucleotides

in SEQ ID NOS: 37 to 54 shall come within the scope of the invention.

In a similar manner, any protein that is produced by these modifications comprising insertion or deletion of one or plural
5 nucleotides and/or substitution with other nucleotides shall come within the scope of the present invention, as far as said protein possesses the activity of the corresponding protein having the amino acid sequence of SEQ ID NOS: 1 to 18.

The cDNAs of the invention include cDNA fragments (more
10 than 10 bp) containing any partial nucleotide sequence of the nucleotide sequence of SEQ ID NOS: 19 to 36 or of the nucleotide sequence of SEQ ID NOS: 37 to 54. Also, DNA fragments consisting of a sense chain and an anti-sense chain shall come within this scope. These DNA fragments can be used
15 as the probes for the gene diagnosis.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are
20 derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or
25 suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate

genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

- 5 Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave
- 10 the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that
- 15 have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified
- 20 genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to
- 25 the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through

insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 5 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 10 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the 15 corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention 20 also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be 25 identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at

least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined
5 by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more,
10 most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and
15 proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of
20 skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the
25 disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

The invention also includes polynucleotides with sequences

complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably
5 highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example,
10 conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 2

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B *; 1×SSC	T _B *; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D *; 1×SSC	T _D *; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F *; 1×SSC	T _F *; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H *; 4×SSC	T _H *; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J *; 4×SSC	T _J *; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L *; 2×SSC	T _L *; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N *; 6×SSC	T _N *; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P *; 6×SSC	T _P *; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R *; 4×SSC	T _R *; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C)=81.5 + 16.6(log₁₀[Na⁺]) + 0.41 (%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory

5 Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

10 Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least
15 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is
20 determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

25 EXAMPLE

The present invention is embodied in more detail by the following examples, but this embodiment is not intended to restrict the present invention. The basic operations and the enzyme reactions with regard to the DNA recombination are

carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restrictive enzymes and a variety of modification enzymes to be used were those available from
5 Takara Shuzo Co., Ltd. The manufacturer's instructions were used for the buffer compositions as well as for the reaction conditions, in each of the enzyme reactions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

10 (1) Preparation of Poly(A)⁺ RNA

The epidermoid carcinoma cell line KB (ATCC CRL 17), tissues of stomach cancer delivered by the operation, and liver were used for human cells to extract mRNAs. The cell line was cultured by a conventional procedure.

15 After about 1 g of human tissues was homogenized in 20 ml of a 5.5 M guanidinium thiocyanate solution, total mRNAs were prepared in accordance with the literature [Okayama, H. et al., "Methods in Enzymology" Vol. 164, Academic Press, 1987]. These mRNAs were subjected to chromatography using an oligo(dT)-
20 cellulose column washed with 20 mM Tris-hydrochloric acid buffer solution (pH 7.6), 0.5 M NaCl, and 1 mM EDTA to obtain a poly(A)⁺ RNA in accordance with the above-mentioned literature.

(2) Construction of cDNA Library

25 To a solution of 10 µg of the above-mentioned poly(A)⁺ RNA in 100 mM Tris-hydrochloric acid buffer solution (pH 8) was added one unit of an RNase-free, bacterium-origin alkaline phosphatase and the resulting solution was allowed to react at 37°C for one hour. After the reaction solution underwent the

phenol extraction followed by the ethanol precipitation, the obtained pellets were dissolved in a mixed solution of 50 mM sodium acetate (pH 6), 1 mM EDTA, 0.1% 2-mercaptoethanol, and 0.01% Triton X-100. Thereto was added one unit of a tobacco-
5 origin pyrophosphatase (Epicenter Technologies) and the resulting solution at a total volume of 100 μ l was allowed to react at 37°C for one hour. After the reaction solution underwent the phenol extraction followed by the ethanol precipitation, the thus-obtained pellets were dissolved in
10 water to obtain a decapped poly(A)⁺ RNA solution.

To a solution of the decapped poly(A)⁺ RNA and 3 nmol of a DNA-RNA chimeric oligonucleotide (5'-dG-dG-dG-dG-dA-dA-dT-dT-dC-dG-dA-G-G-A-3') in a mixed aqueous solution of 50 mM Tris-hydrochloric acid buffer solution (pH 7.5), 0.5 mM ATP, 5 mM
15 MgCl₂, 10 mM 2-mercaptoethanol, and 25% polyethylene glycol were added 50 units of T4 RNA ligase and the resulting solution at a total volume of 30 μ l was allowed to react at 20°C for 12 hours. After the reaction solution underwent the phenol extraction followed by the ethanol precipitation, the thus-
20 obtained pellets were dissolved in water to obtain a chimeric oligo-capped poly(A)⁺ RNA.

After the vector pKA1 developed by the present inventors (Japanese Patent Kokai Publication No. 1992-117292) was digested with KpnI, an about 60-dT tail was inserted by a
25 terminal transferase. This product was digested with EcoRV to remove the dT tail at one side and the resulting molecule was used as a vectorial primer.

After 6 μ g of the previously-prepared chimeric oligo-capped poly(A)⁺ RNA was annealed with 1.2 μ g of the vectorial

primer, the product was dissolved in a mixed solution of 50 mM Tris-hydrochloric acid buffer solution (pH 8.3), 75 mM KCl, 3 mM MgCl₂, 10 mM dithiothreitol, and 1.25 mM dNTP (dATP + dCTP + dGTP + dTTP), mixed with 200 units of a reverse transferase
5 (GIBCO-BRL), and the resulting solution at a total volume of 20 µl was allowed to react at 42°C for one hour. After the reaction solution underwent the phenol extraction followed by the ethanol precipitation, the thus-obtained pellets were dissolved in a mixed solution of 50 mM Tris-hydrochloric acid
10 buffer solution (pH 7.5), 100 mM NaCl, 10 mM MgCl₂, and 1 mM dithiothreitol. Thereto were added 100 units of EcoRI and the resulting solution at a total volume of 20 µl was allowed to react at 37°C for one hour. After the reaction solution underwent the phenol extraction followed by the ethanol
15 precipitation, the obtained pellets were dissolved in a mixed solution of 20 mM Tris-hydrochloric acid buffer solution (pH 7.5), 100 mM KCl, 4 mM MgCl₂, 10 mM (NH₄)₂SO₄, and 50 µg/ml bovine serum albumin. Thereto were added 60 units of *Escherichia coli* DNA ligase and the resulting solution was
20 allowed to react at 16°C for 16 hours. To the reaction solution were added 2 µl of 2 mM dNTP, 4 units of *Escherichia coli* DNA polymerase I, and 0.1 unit of *Escherichia coli* DNase H and the resulting solution was allowed to react at 12°C for one hour and then at 22°C for one hour.

25 Next, the cDNA-synthesis reaction solution was used to transform *Escherichia coli* DH12S (GIBCO-BRL). The transformation was carried out by the electroporation method. A portion of the transformant was inoculated on a 2xYT agar culture medium containing 100 µg/ml ampicillin, which was

incubated at 37°C overnight. A colony grown on the culture medium was randomly picked up and inoculated on 2 ml of the 2xYT culture medium containing 100 µg/ml ampicillin, which was incubated at 37°C overnight. The culture medium was centrifuged to separate the cells, from which a plasmid DNA was prepared by the alkaline lysis method. After the plasmid DNA was double-digested with EcoRI and NotI, the product was subjected to 0.8% agarose gel electrophoresis to determine the size of the cDNA insert. In addition, by the use of the obtained plasmid as a template, the sequence reaction using M13 universal primer labeled with a fluorescent dye and Taq polymerase (a kit of Applied Biosystems Inc.) was carried out and the product was analyzed by a fluorescent DNA-sequencer (Applied Biosystems Inc.) to determine the base sequence of the cDNA 5'-terminal of about 400 bp. The sequence data were filed as a homo-protein cDNA bank data base.

(3) Selection of cDNAs Encoding Proteins Having Transmembrane Domains

The base sequence registered in the homo-protein cDNA bank data base was converted to three frames of amino acid sequences and the presence or absence of an open reading frame (ORF) beginning from the initiation codon. Then, the selection was made for the presence of a signal sequence that is characteristic to a secretory protein at the N-terminal of the portion encoded by ORF. These clones were sequenced from the both 5' and 3' directions by using the deletion method to determine the sequence of the whole base sequence. The hydrophobicity/hydrophilicity profiles were obtained for proteins encoded by ORF by the Kyte-Doolittle method [Kyte, J.

& Doolittle, R. F., J. Mol. Bio. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic region. In the case in which there is a hydrophobic region of putative transmembrane domain(s) in the amino acid sequence of an encoded protein, this protein was considered as a membrane protein.

(4) Construction of Secretory Signal Detection Vector pSSD3

One microgram of pSSD1 carrying the SV40 promoter and a cDNA encoding the protease domain of urokinase [Yokoyama-Kobayashi, M. et al., Gene 163: 193-196 (1995)] was digested with 5 units of BglII and 5 units of EcoRV. Then, after dephosphorylation at the 5' terminal by the CIP treatment, a DNA fragment of about 4.2 kbp was purified by cutting off from the gel of agarose gel electrophoresis.

Two oligo DNA linkers, L1 (5'-GATCCCGGGTCACGTGGGAT-3') and L2 (5'-ATCCACGTGACCCGG-3'), were synthesized and phosphorylated by T4 polynucleotide kinase. After annealing of the both linkers, followed by ligation with the previously-prepared pSSD1 fragment by T4 DNA ligase, *Escherichia coli* JM109 was transformed. A plasmid pSSD3 was prepared from the transformant and the objective recombinant was confirmed by the determination of the base sequence of the linker-inserted fragment. Figure 1 illustrates the structure of the thus-obtained plasmid. The present plasmid vector carries three types of blunt-end formation restriction enzyme sites, SmaI, PmaCI, and EcoRV. Since these cleavage sites are positioned in succession at an interval of 7 bp, selection of an appropriate site in combination of three types of frames for the inserting

cDNA allows to construct a vector expressing a fusion protein.

(5) Functional Verification of Secretory Signal Sequence

Whether the N-terminal hydrophobic region in the secretory protein clone candidate obtained in the above-mentioned steps functions as the secretory signal sequence was verified by the method described in the literature [Yokoyama-Kobayashi, M. et al., Gene 163: 193-196 (1995)]. First, the plasmid containing the target cDNA was cleaved at an appropriate restriction enzyme site that existed at the downstream of the portion expected for encoding the secretory signal sequence. In the case in which this restriction enzyme site was a protruding terminus, the site was blunt-ended by the Klenow treatment or treatment with the mung-bean nuclease. Digestion with HindIII was further carried out and a DNA fragment containing the SV40 promoter and a cDNA encoding the secretory sequence at the downstream of the promoter was separated by agarose gel electrophoresis. This fragment was inserted between the pSSD3 HindIII site and a restriction enzyme site selected so as to match with the urokinase-coding frame, thereby constructing a vector expressing a fusion protein of the secretory signal portion of the target cDNA and the urokinase protease domain.

After *Escherichia coli* (host: JM109) bearing the fusion-protein expression vector was incubated at 37°C for 2 hours in 2 ml of the 2xYT culture medium containing 100 µg/ml ampicillin, the helper phage M13K07 (50 µl) was added and the incubation was continued at 37°C overnight. A supernatant separated by centrifugation underwent precipitation with polyethylene glycol to obtain single-stranded phage particles. These particles were suspended in 100 µl of 1 mM Tris-0.1 mM

EDTA, pH 8 (TE). Also, there was used as a control a suspension of single-stranded particles prepared in the same manner from the vector pLA1-UPA containing pSSD3 and a full-length cDNA of urokinase [Yokoyama-Kobayashi, M. et al., Gene 163: 193-196
5 (1995)].

The simian-kidney-origin culture cells, COS7, were incubated at 37°C in the presence of 5% CO₂ in the Dulbecco's modified Eagle's culture medium (DMEM) containing 10% bovine fetus albumin. Into a 6-well plate (Nunc Inc., 3 cm in the well
10 diameter) were inoculated 1×10^5 COS7 cells and incubation was carried out at 37°C for 22 hours in the presence of 5% CO₂. After the culture medium was removed, the cell surface was washed with a phosphate buffer solution and then washed again with DMEM containing 50 mM Tris-hydrochloric acid (pH 7.5)
15 (TDMEM). To the cells were added 1 µl of the single-stranded phage suspension, 0.6 ml of the DMEM culture medium, and 3 µl of TRANSFECTAM™ (IBF Inc.) and the resulting mixture was incubated at 37°C for 3 hours in the presence of 5% CO₂. After the sample solution was removed, the cell surface was washed
20 with TDMEM, 2 ml per well of DMEM containing 10% bovine fetus albumin was added, and the incubation was carried out at 37°C for 2 days in the presence of 5% CO₂.

To 10 ml of 50 mM phosphate buffer solution (pH 7.4) containing 2% bovine fibrinogen (Miles Inc.), 0.5% agarose, and
25 1 mM potassium chloride were added 10 units of human thrombin (Mochida Pharmaceutical Co., Ltd.) and the resulting mixture was solidified in a plate of 9 cm in diameter to prepare a fibrin plate. Ten microliters of the culture supernatant of the

transfected COS7 cells were spotted on the fibrin plate, which was incubated at 37°C for 15 hours. The diameter of the thus-obtained clear circle was taken as an index for the urokinase activity. In the case in which a cDNA fragment codes for the amino acid sequence that functions as a secretory signal sequence, a fusion protein is secreted to form a clear circle by its urokinase activity. Therefore, in the case in which a clear circle is not formed, the fusion protein remains as trapped in the membrane and the cDNA fragment is considered to code for a transmembrane domain.

(6) Protein Synthesis by In Vitro Translation

The plasmid vector carrying the cDNA of the present invention was utilized for the transcription/translation by the T_NT rabbit reticulocyte lysate kit (Promega Biotec). In this case, [³⁵S]methionine was added and the expression product was labeled with the radioisotope. All reactions were carried out by following the protocols attached to the kit. Two micrograms of the plasmid was allowed to react at 30°C for 90 minutes in total 25 ml of a reaction solution containing 12.5 µl of the T_NT rabbit reticulocyte lysate, 0.5 µl of the buffer solution (attached to the kit), 2 µl of an amino acid mixture (methionine-free), 2 µl (0.37 MBq/µl) of [³⁵S]methionine (Amersham Corporation), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. To 3 µl of the reaction solution was added 2 µl of an SDS sampling buffer (125 mM Tris-hydrochloric acid suffer solution, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue, and 20% glycerol) and the resulting solution was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis. The molecular weight of

the translation product was determined by carrying out the autoradiography.

(7) Expression in COS7

Escherichia coli bearing a vector expressing the protein
 5 of the invention was infected with helper phage M13K07, and
 single-stranded phage particles were obtained according to the
 method as stated above. Using the thus obtained phages, each
 expression vecotr was introduced into simian-kidney-origin
 culture cells COS7 in the manner as stated above. After
 10 incubation at 37 °C for 2 days in the presence of 5 % CO₂,
 further incubation was carried out in a medium containing
 [³⁵S]cysteine or [³⁵S]methionine for 1 hour. The cells were
 collected, dissolved and then subjected to SDS-PAGE whereby a
 band corresponding to the expression product of each protein
 15 which is not present in COS7 cells was revealed. In Table 3,
 the molecular weight of each expression product is shown.

Table 3

20	HP Number	Supernatant of culture	Membrane fraction
		(kDa)	(kDa)
	HP01263	50	-
	HP01299	-	30
	HP01526	-	22
25	HP10230	-	24
	HP10408	-	7
	HP10415	-	45
	HP10424	-	14
	HP10429	-	27
30	HP10432	-	17
	HP10480	-	22

(8) Clone Examples

<HP01263> (Sequence Number 1, 19, 37)

Determination of the whole base sequence for the cDNA insert of clone HP01263 obtained from the human liver cDNA
5 libraries revealed the structure consisting of a 5'-non-translation region of 36 bp, an ORF of 1149 bp, and a 3'-non-translation region of 316 bp. The ORF codes for a protein consisting of 382 amino acid residues with one transmembrane domain at the N-terminal. Figure 2 depicts the hydrophobicity
10 /hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in formation of a translation product of 42 kDa, which is almost consistent with the molecular weight of 42,054 as predicted from the ORF. On expression in COS cells, an expression
15 product of about 50 kDa was observed in the culture supernatant. Therefore, said protein can be understood to be a secreted protein. Application of the rule (-3, -1) as a method for anticipation of a cutting site in a secretion signal sequence suggested that the mature protein would start from
20 methionine at 19 position.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the human α -2-HS-glycoprotein (SWISS-PROT Accession No. P02765). Table 4 indicates the comparison of the
25 amino acid sequences between the human protein of the present invention (HP) and the human α -2-HS-glycoprotein (GP). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the

protein of the present invention. The both proteins possessed a homology of 25.5%. The cysteine position is reserved and this region is analogous to that in cystatins (thiol proteinase inhibitors). There are observed other analogy with histidine-rich glycoprotein (P04196, 30.9%/194 amino acid residues), kininogen (P01045, 24.1%/261 amino acid residues), tyrosine kinase inhibitor (A32827, 24.4%/291 amino acid residues), and so on.

Table 4

10

HP	MGLLLPLALCILVLCGGAMSPQALNPSALLSR--GCNDSVDLAVAGFALRDINKDRKD
	.*** * . . . * . * . * . . . * . * . *
GP	MKSLVLLLCLAQLWGCHSAPHGPGLIYRQPNCDDEPETEEAALVAIDYINQNLFW
HP	GYVLRRLNRVNDAAQEYRRGGLGSLFYLTLDVLETDCHVLRKKAWQDCGMRIFFE-SVYQC
15	** **..... ** ...*...***** .. . *... * . * **
GP	GKHTLNQIDEVKVWPQPSGELFEIEIDTLETTCHVLDPTPVARCSVRQLKEHAVEGDC
HP	K-AIFYMNNPSRVLYLAAYNCTLRPVSKKKIYMTCPDCPSSIPTDSSNHQVLEAATESLA
 *.* . * . * * . . . * . * . * . * . *
GP	DFQLKLDGKFSVVY---AKCDSSPDSAEDVRKVCQDCPLLAPLN--DTRVVHAAKAALA
20	HP KYNNESTSKQYSLFKVTRASSQWVVGPSYFVEYLKESPC---TKSQASSCSLQSSDSVP
	. * . * . . . * . . * . . * . * . . . * . * . . . * . *
GP	AFNAQNNGSNFQLEEISRAQLV-PLPPSTYVEFTVSGTDCVAKEATEAAKCNLLAEKQY-
HP	VGLCKGSLTRTHWEKFVSVTCDFEFESQAPATGSESAVNQK-PTNLPKVEESQKNTPT
	* . * . * . . . * . * . * . . . * . * . * . . . *
25	GP -GFCKATLSEKLGAEVAVTCTVFQTQPVTSQPQPEGANEAVPTPVVDPDAPPSPLGAP
HP	DSPSKAGPRGSVQYLPDLDDKNSQEKGPQEAFFVHLDLTNPQGETLDISFLFLEPMEEK
	. * . * . * . * . *
GP	GLPPAGSPDSHVLLAAPPQHQLHRAHYDLRHTFMGVVSLGSPSGEVSHPRKTRTVVQPS
HP	LVVLPFPKEKARTAECPGAQNASPLVLPP
30	GP VGAAAGPVVPPCPGRIRHFKV

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. H57204), but it can not be assessed whether these ESTs with
5 partial sequences code for the same protein as the protein of the present invention. Hereupon, most of ESTs matching with the present cDNA are available from liver cDNA libraries, whereby the present clone is considered to be expressed specifically in the liver.

10 The present protein, because of being a type-II membrane protein, is considered to exert its function as a receptor on the membrane surface with the C-terminal side exposed outside the cells or after undergoing a processing followed by being excreted in the serum. The present protein, because of bearing
15 a cystatin-like domain, is considered to possess a proteinase-inhibitor activity as well as many physiological activities in the same manner as for other members of this family. In addition, the present protein, because of being expressed specifically in liver cells, is considered to play a
20 significant role for maintaining the liver function.

<HP01299> (Sequence Number 2, 20, 38)

Determination of the whole base sequence for the cDNA insert of clone HP01299 obtained from the human liver cDNA libraries revealed the structure consisting of a 5'-non-
25 translation region of 110 bp, an ORF of 954 bp, and a 3'-non-translation region of 285 bp. The ORF codes for a protein consisting of 317 amino acid residues with two or more transmembrane domains. Figure 3 depicts the hydrophobicity/hydrophilicity profile of the present protein

obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 32 kDa that was almost consistent with the molecular weight of 35,965 predicted from the ORF.

5 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the rat retinol dehydrogenase (NBRF Accession No. A55884). Table 5 indicates the comparison of the amino acid sequences between the human protein of the present invention
10 (HP) and the rat retinol dehydrogenase (RN). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and. represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 65.3%
15 among the entire regions.

Table 5

	HP	MWLYLAAFVGLYLLHWYRERQVVSHLQDKYVFITGCDSGFGNLLARQLDARGLRVLAAC
5		***** *.***. **. ****.***** ***** **.******
	RN	MWLYLLALVGLWNLLRLFRERKVVSHLQDKYVFITGCDSGFGNLLARQLDRRGMRVLAAC
	HP	LTEKGAEQLRGQTSRLETVTLDVTKMESIAAATQWVKEHVGDRGLWGLVNNAGILTPIT
		*****.*****.***** ***.*****.***.***** ***** .*..
	RN	LTEKGAEQLRSKTSRLETVILDVTKTESIVAATQWVKERVGNRGLWGLVNNAGISVPVG
10	HP	LCEWLNTEDSMNMLKVNLIQVITLSMLPLVRRARGRIVNVSSILGRVAFFVGGYCVSK
	* ..*.*.***.***.*****.*****.***.***.***.***.***.***
	RN	PNEWMRKKDFASVLDVNLLGVIEVTLNMLPLVRKARGRVVNIASMTGRMSLVGGGYCISK
	HP	YGVEAFSDILRREIQHFGVKISIVEPGYFRTGMTNMTQSLERMQSWKEAPKHIKETYGQ
		***** *****. *****.***.***.***.***.***.***.***.***.***.***
15	RN	YGVEAFSDSLRRELTYFGVKVAIIIEPGGFKTNVTNMERLSDNLKKLWDQTTEEVKEIYGE
	HP	QYFDALYNIMKEGLLNCSTNLNLVTDCEHALTSVHPRTSYSAGWDKFFFIPLSYLPTS
		.. *. . *.. . ***.***.***** *****.*****.***.*****
	RN	KFQDSYMKAMESLVNTCSGDSLVTDCMEHALTSCHPRTRYSPGWDKFFYLPM sylPTF
	HP	LADYILTRSWPKPAQAV
20		*.* ***.*.
	RN	LSDAVIHGWSVKPARAL

Furthermore, the search of GenBank using the base sequence
 25 of the present cDNA revealed that there existed some ESTs
 possessing the homology of 90% or more (for example, Accession
 No. R35197), but any of them was shorter than the present cDNA
 and did not contain the initiation codon.

The rat retinol dehydrogenase has been found as a
 30 microsomal membrane protein participating in the retinoic acid

biosynthesis in the liver [Chai, X. et al., J. Biol. Chem. 270: 28408-28412 (1995)]. Accordingly, its homologue, the protein of the present invention, is considered to possess a similar function and can be utilized for diagnosis and treatment of diseases caused by the abnormality of this protein.

<HP01347> (Sequence Number 3, 21, 39)

Determination of the whole base sequence for the cDNA insert of clone HP01347 obtained from the human liver cDNA libraries revealed the structure consisting of a 5'-non-translation region of 24 bp, an ORF of 891 bp, and a 3'-non-translation region of 728 bp. The ORF codes for a protein consisting of 296 amino acid residues with one transmembrane domain at the N-terminal. Figure 4 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified and the urokinase activity was detected on the membrane surface, upon transduction into the COS7 cells of an expression vector in which a HindIII-SacI fragment (treated with the mung-bean nuclease) containing a cDNA fragment encoding the N-terminal 73 amino acid residues in the present protein was inserted at the HindIII-EcoRV site of pSSD3. Therefore, the present protein is considered to be a type-II membrane protein. The in vitro translation resulted in the formation of a translation product of 33 kDa that was almost consistent with the molecular weight of 33,527 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was

analogous to the human HIV envelope glycoprotein gp120-binding C-type lectin (GenBank Accession No. M98457). Table 6 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the human HIV
5 envelope glycoprotein gp120-binding C-type lectin (CL). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed
10 a homology of 85.6% among 284 amino acid residues. There is observed at the downstream of the transmembrane domain a sequence with seven repetition of Ile-Tyr-Gln-Xaa-Leu-Thr-Xaa-Leu-Lys-Ala-Ala-Val-Gly-Glu-Leu-Xaa-Xaa-Xaa-Ser-Lys-Xaa-Gln-Xaa.

Table 6

	HP	MSDSKEPRVQQLGLL-----GCLGHGALVLQLLSFMLLAGVLVAI
		*****.***** *****.***** *****
5	CL	MSDSKEPRLQQLGLLEEEQLRGLGFRQTRGYKSLAGCLGHGPLVLQLLSFTLLAG----L
	HP	LVQVSKVPSSLSQEQSEQDAIYQNLTLKAAVGELSEKSKLQEIYQELTQLKAAVGELPE
		*****.***** *****
	CL	LVQVSKVPSSISQEQSRQDAIYQNLTLKAAVGELSEKSKLQEIYQELTQLKAAVGELPE
	HP	KSKLQEIYQELTRLKAAVGELPEKSKLQEIYQELTRLKAAVGELPEKSKLQEIYQELTRL
10		*****.*****.*****
	CL	KSKLQEIYQELTRLKAAVGELPEKSKLQEIYQELTWLKAAVGELPEKSKMQEIYQELTRL
	HP	KAAVGELPEKSKLQEIYQELTELKAAVGELPEKSKLQEIYQELTQLKAAVGELPDQSKQQ
		***** ***** ***** *****.*****.*****
	CL	KAAVGELPEKSKQEIYQELTRLKAAVGELPEKSKQEIYQELTRLKAAVGELPEKSKQQ
15	HP	QIYQELTDLKTAFERLCRHCPEKDWTFQGNFCYFMSNSQRNWHDSVTACQEVRAQLVVIKT
		.*****.***.*****.*****.*****.*****.*****.*****.*****.*****
	CL	EIYQELTQLKAAVERLCHPCPWEWTFQGNFCYFMSNSQRNWHDSITACKEVGAQLVVIKS
	HP	AEEQLPAVLEQWRTQQ
		**** *. *...
20	CL	AEEQNFLQLQSSRSNRFTWMGLSDLNQEGTWQWVDGSPLLPSFKQYWNRGEPNNVGEEDC

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. H90360), but it can not be assessed whether these ESTs with partial sequences code for the same protein as the protein of the present invention.

The present protein, because of being a type-II membrane protein, is considered to exert its function as a receptor on

the membrane surface with the C-terminal side exposed outside the cells or after undergoing a processing followed by being excreted in the serum. Hereupon, the human HIV envelope glycoprotein gp120-binding C-type lectin that is highly homologous with the present protein has been found as a CD4-independent HIV receptor [Curtis, B. M. et al., Proc. Natl. Acad. Sci. USA 89: 8356-8360 (1992)].

<HP01440> (Sequence Number 4, 22, 40)

Determination of the whole base sequence for the cDNA insert of clone HP01440 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 37 bp, an ORF of 594 bp, and a 3'-non-translation region of 98 bp. The ORF codes for a protein consisting of 197 amino acid residues with four transmembrane domains. Figure 5 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 21 kDa that was almost consistent with the molecular weight of 20,822 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the human tumor-associated antigen L6 (SWISS-PROT Accession No. P30408). Table 7 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the human tumor-associated antigen L6 (L6). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed

a homology of 47.0% among the entire regions.

Table 7

5	HP	MCTGKCARCVGLSLITLCLVCIVANALLVPNGETSWTNTNHLQLQVWLMGGFIGGGLMV
		** *****.* **..* *.**.* ** *****.....** **..*..*****..
	L6	MCYGKCARCIGHSLVGLALLCIAANILLYFPNGETKYASENHLRFVWFFSGIVGGGLLM
	HP	LCPG---IAAVRAGGKCGCGAGCCGNRCMLRSVFSSAFGLGAIYCLSVSGAGLRNGPR
		* *. * **** . **.* **.*... *. *. **.* .. ** .**
10	L6	LLPAFVFIGLEQDDCCCGCGHENCCKRCAMLSSVLAALIGIAGSGYCVIVAALGLAEGPL
	HP	CLMN-GEWGYHFEDTAGAYLLNRTLWDRCEAPPRVVPWNVTLSLLVAASCLEIVLCGIQ
		** . *.*.* **.*.***. . *. *..* ..* ***.***.*. . .**.* **
	L6	CLDSLQWNYTFASLEGQYLLDTSTWSECTEPKHIVEWNVSLFSILLALGGIEFILCLIQ
	HP	LVNATIGVFCGDCRKKQDTPH
15		..*..* .** * ..*.
	L6	VINGVLGGICGFCCSHQQQYDC

Furthermore, the search of GenBank using the base sequence
 20 of the present cDNA revealed that there existed some ESTs
 possessing the homology of 90% or more and also containing the
 initiation codon (for example, Accession No. T55097), but many
 sequences were not distinct and the same ORF as that in the
 present cDNA was not identified.

25 The human tumor-associated antigen L6 is a member of a
 membrane antigen TM4 superfamily proteins which are expressed
 in large quantities on the surface of human tumor cells
 [Marken, J. S. et al., Proc. Natl. Acad. Sci. USA 89: 3503-3507
 (1992)]. Since these membrane antigens are expressed
 30 specifically on some specified cells or cancer cells,

antibodies against these antigens, if constructed, are useful for a variety of diagnoses and as carriers for the drug delivery. In addition, the cells in which genes of these membrane antigens are transduced and the membrane antigens are
5 expressed are applicable for detection of the corresponding ligands and so on.

<HP01526> (Sequence Number 5, 23, 41)

Determination of the whole base sequence for the cDNA insert of clone HP01526 obtained from the human stomach cancer
10 cDNA libraries revealed the structure consisting of a 5'-non-translation region of 83 bp, an ORF of 666 bp, and a 3'-non-translation region of 573 bp. The ORF codes for a protein consisting of 221 amino acid residues with a hydrophobic region of putative six transmembrane domains. Figure 6 depicts the
15 hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 23 kDa that was almost consistent with the molecular weight of 25,030 predicted from the ORF.

20 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the mouse interstitial cell protein (GenBank Accession No. X96618). Table 8 indicates the comparison of the amino acid sequences between the human protein of the present
25 invention (HP) and the mouse interstitial cell protein (MM). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed

a homology of 79.6% among the entire regions.

Table 8

5	HP	MEAGGF LDSLIYGACVVFTLGMFSAGLSDLRHRMTRSDNVQFLPFLTTEVNNLCWLSY
		***** **.. .***.*****.*****.*****.*****.*****.*****.*****
	MM	MEAGGVADSF LSSACVLFTLGMFSTGLSDLRHMQRTRSDNIQFLPFLT TDVNNLSWLSY
	HP	GALKGDGILIVNTVGAALQTLYLAYLHYCPKRKVLLQTATLLGVLLLG YGYFWLLVP
		*.*****.***.***.***.*****.***.***.*****.*****.*****.*****
10	MM	GVLKGDGTLIIVNSVGAVLQTLYLAYLHYSPQKHGVLLQTATLLAVLLLG YGYFWLLVP
	HP	NPEARLQQLGLFCSVFTISMYLSPLADLAKVIQTKSTQCLSYP LTIATLLTSASWCYGYF
		. *****.*****.*****.*****.*****.*****.*****.*****.*****
	MM	DLEARLQQLGLFCSVFTISMYLSPLADLAKIVQTKSTQRLSFSLTIATL FCSASWSIYGYF
	HP	RLRDPYIMVSNFFGIVTSFIRFWLFWKYPQEQDRNYWLLQT
15		***** *.***.***.***.***.***.***.***.***.***.***.***.***.***.***
	MM	RLRDPYIAVPNLPGILTSLIRLGLFCKYPPEQDRKYRLLQT

Furthermore, the search of GenBank using the base sequence
 20 of the present cDNA revealed that there existed some ESTs
 possessing the homology of 90% or more and also containing the
 initiation codon (for example, Accession No. H02682), but many
 sequences were not distinct and the same ORF as that in the
 present cDNA was not identified.

25 The mouse interstitial cell protein has been cloned as a
 membrane protein that is expressed with highly increasing in
 interstitial cells stimulated by a cytokine [Tagoh, H. et al.,
 Biochem. Biophys. Res. Commun. 221: 744-749 (1996)]. Since
 these membrane proteins are expressed specifically on some
 30 specified cells and cancer cells, antibodies against these

proteins, if constructed, are useful for a variety of diagnoses and as carriers for the drug delivery. In addition, the cells in which genes of these membrane antigens are transduced and the membrane antigens are expressed are applicable for
5 detection of the corresponding ligands and so on.

<HP10230> (Sequence Number 6, 24, 42)

Determination of the whole base sequence for the cDNA insert of clone HP10230 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-
10 translation region of 190 bp, an ORF of 756 bp, and a 3'-non-translation region of 2099 bp. The ORF codes for a protein consisting of 251 amino acid residues with at least one transmembrane domain. Figure 7 depicts the hydrophobicity/hydrophilicity profile of the present protein
15 obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 30 kDa that was almost consistent with the molecular weight of 28,800 predicted from the ORF.

The search of the protein data base using the amino acid
20 sequence of the present protein revealed that the protein was analogous to the nematode hypothetical protein F25D7.1 (GenBank Accession No. Z78418). Table 9 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the nematode hypothetical protein F25D7.1
25 (CE). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 49.8% among the entire regions.

Table 9

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HS  MSDIGDWFRSIPAITRYWFAATVAVPLVGKGLISPAYLFL-WPEAFLYRFQIWRPITAT
      *..... ** .***** *.. **.***.***. ....** * . . **.****.*
5  CE  MDLENFLLGIPIVTRYWFLASTIIPLLGRFGFINVQWMFLQW-DLVVNKFQFWRPLTAL
HS  FYFPVPGPTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNW-ICIVITGLAMDM
      *.***.* *** *. *****. **.... **.*****.*** * . .***.
CE  IYYPVTPQTGFHWLMMCYFLYNYSKALESETYGRSADYLFMLIFNWFFCSGLC-MALDI
HS  QLLMIPLIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNL
10   *. *...***** *.*. * ***** ** * *****. *** .. *. ****.* *
CE  YFLEPMVISVLYVWCQVNKDTIVSFWFGMRFPARYLPWVLWGFNAVLRGGGTNELVGIL
HS  VGHLYFFLMFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPASMERAADQNGGGG
      *** ***. ..** . * ...***.***. *. **.* * * * *
CE  VGHAYFFVALKYPDEYGV-DLISTPEFLHRLIPDEDGGIGHG---QDGNIRGARQQPRG--
15 HS  RHNW--GQGFR LGDQ
      * * * * ***
CE  -HQWPGGVGARLGGN

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20 Furthermore, the search of GenBank using the base sequence
of the present cDNA revealed that there existed some ESTs
possessing the homology of 90% or more and also containing the
initiation codon (for example, Accession No. W01493), but many
sequences were not distinct and the same ORF as that in the
25 present cDNA was not identified.

<HP10389> (Sequence Number 7, 25, 43)

Determination of the whole base sequence for the cDNA insert of clone HP10389 obtained from the human epidermoid carcinoma cell line KBc cDNA libraries revealed the structure consisting of a 5'-non-translation region of 62 bp, an ORF of

321 bp, and a 3'-non-translation region of 270 bp. The ORF codes for a protein consisting of 106 amino acid residues with a hydrophobic region of putative two transmembrane domains. Figure 8 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 12 kDa that was almost consistent with the molecular weight of 11,528 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any of known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. H70816), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

<HP10408> (Sequence Number 8, 26, 44)

Determination of the whole base sequence for the cDNA insert of clone HP10408 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 74 bp, an ORF of 237 bp, and a 3'-non-translation region of 128 bp. The ORF codes for a protein consisting of 78 amino acid residues with a putative signal sequence at the N-terminal as well as a sequence of one putative interior transmembrane domain. Figure 9 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified

upon transduction into the COS7 cells of an expression vector in which a HindIII-BglII fragment (after the Klenow treatment) containing a cDNA fragment encoding the N-terminal 70 amino acid residues in the present protein was inserted at the
5 HindIII-EcoRV site of pSSD3. The in vitro translation resulted in the formation of a translation product of 9 kDa that was almost consistent with the molecular weight of 8,396 predicted from the ORF.

Furthermore, the search of GenBank using the base sequence
10 of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. T94049), but they were shorter than the present cDNA and any molecule containing the initiation codon was not identified.

15 <HP10412> (Sequence Number 9, 27, 45)

Determination of the whole base sequence for the cDNA insert of clone HP10412 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 55 bp, an ORF of 945 bp, and a 3'-non-translation region of 131 bp. The ORF codes for a protein
20 consisting of 314 amino acid residues with one transmembrane domain at the N-terminal. Figure 10 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that
25 the present protein remained in the membrane from the observation that the urokinase secretion was not identified upon transduction into the COS7 cells of an expression vector in which a HindIII-ApaI fragment (treated with mung-bean nuclease) containing a cDNA fragment encoding the N-terminal 65

amino acid residues in the present protein was inserted at the HindIII-EcoRV site of pSSD3. The in vitro translation resulted in the formation of a translation product of 44 kDa that was somewhat larger than the molecular weight of 35,610 predicted
5 from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the nematode hypothetical protein of 28.5 kDa (SWISS-PROT Accession No. P34623). Table 10 indicates the
10 comparison of the amino acid sequences between the human protein of the present invention (HP) and the nematode hypothetical protein of 28.5 kDa (CE). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino
15 acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 42.8% in the C-terminal region of 243 amino acid residues.

Table 10

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HP   MVAPVWYLVA AALLVG FILFLTRSRGRAASAGQEPLHNEELAGAGRVAQPGPLEPEEPRA
5    HP   GGRPRRRRDLG SRLQAQRRAQRVAWAEA--DENEEEA VILA QEEEGVEKPAETHLSGKIG
      * .*.***.* . . . . . . . . . . *. * . . . . ***
CE           MRRNARRRVNRDEQEDG FVNHMNDGEDVEDLDGGAEQFEYDEDGKKIG
HP   AKKLRLKEEKQARKAQREAEAAEREERKRLESQREA EWKKEEERLRLEEEQKEEEE--RK
      .* **..*..... ** * ***** *..* * *..*** . *...*.*** **
10   CE   KRKA AKLQAKEE KRMREYEVREREERKRREEER--EK RDEERAKEEAD EKAEEERLRK
HP   AREEQ AQREHEE YLKLKEAFVVEEGVG ETMTTEE QSQSFLT EFINYIKQSKVVLLEDLAS
      .***....***** . *...***** .....*..... . *..*.* .*** ...*.*
CE   EREEKERKEHEE YLAMKASF AIEEEG-TDAIEGE EAENLIRDFVDYVKTNKVVNIDELSS
HP   QVGLRTQDTINRIQLLAEGTITGV IDDRGKF IYITPEELA AVANFIRQRGRVSIAELAQ
15     . **...*.**.*.....* . **.*****. **.****.**.***** *.*.
CE   HFGLKSEDA VNRLQHFI EEGLVQGVMD DRGKF IYISDEEF AA VAKFINQRGRVSIHEIAE
HP   ASNSLIAWGRES PAQAPA
      .**.** . *.*.
CE   QSNRLIRLETPSAAE

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Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. T09311), but it can not be assessed whether these ESTs with partial sequences code for the same protein as the protein of the present invention.

<HP10413> (Sequence Number 10, 28, 46)

Determination of the whole base sequence for the cDNA
30 insert of clone HP10413 obtained from the human stomach cancer

cDNA libraries revealed the structure consisting of a 5'-non-translation region of 78 bp, an ORF of 588 bp, and a 3'-non-translation region of 1209 bp. The ORF codes for a protein consisting of 195 amino acid residues with one transmembrane domain at the N-terminal. Figure 11 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified upon transduction into the COS7 cells of an expression vector in which a HindIII-PmaCI fragment containing a cDNA fragment encoding the N-terminal 65 amino acid residues in the present protein was inserted at the HindIII-PmaCI site of pSSD3. The in vitro translation resulted in the formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 21,671 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the swine steroidal membrane-binding protein (GenBank Accession No. X99714). Table 11 indicates the comparison of the amino acid sequences between the human protein of the present invention (HP) and the swine steroidal membrane-binding protein (SS). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The both proteins possessed a homology of 96.4% among the entire regions.

Table 11

	HP	MAAEDVVATGADPSDLESGGILLHEIFTSPNLNLLLGLCIFLLYKIVRGDQPAASGDSDDD
		*****.*****.***.*****
5	SS	MAAEDVAATGADPSELEGGILLHEIFTSPNLNLLLGLCIFLLYKIVRGDQPAAS-DSDDD
	HP	EPPPLPRLKRRDFTPaelRRFDGVQDPRILMAINCKVFDVTKGRKFYGPegPYGVFAGRd

	SS	EPPPLPRLKRRDFTPaelRRFDGVQDPRILMAINCKVFDVTKGRKFYGPegPYGVFAGRd
	HP	ASRGLATFCLdKEALKDEYDDLSDLTAAQETLSDWESQFTFKYHHVGKLLKEGEEPTVY
10		*****.*****.***.*****
	SS	ASRGLATFCLdKEALKDEYDDLSDLTPAQETLNDWDSQFTFKYHHVGKLLKEGEEPTVY
	HP	SDEEEKDESARKND

	SS	SDEEEKDESARKND

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. AA021062), but many sequences were not distinct and the same ORF as that in the present cDNA was not identified.

<HP10415> (Sequence Number 11, 29, 47)

Determination of the whole base sequence for the cDNA insert of clone HP10415 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 71 bp, an ORF of 1389 bp, and a 3'-non-translation region of 103 bp. The ORF codes for a protein consisting of 462 amino acid residues with one transmembrane domain at the N-terminal. Figure 12 depicts the hydrophobicity/hydrophilicity profile of the present protein

obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 48 kDa that was somewhat smaller than the molecular weight of 52,458 predicted from the ORF.

5 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the cytochrome P450 as exemplified by the simian cytochrome P450IIIA8 (SWISS-PROT Accession No. P33268). Table 12 indicates the comparison of the amino acid sequences between
10 the human protein of the present invention (HP) and the simian cytochrome P450IIIA8 (CP). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present invention. The
15 both proteins possessed a homology of 21.3% among the entire regions.

Table 12

	HP	MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVN-SGSLHEF
		.***. * *
5	CP	MDLIPDLAVETWLLAVTLVLLYLYGTHSHGLFKKLIGPPTPLPLGNILSYRKGFWTF
	HP	LVNLHERYGPVVSFWFGRRLVVS LGTVDLKQHINPNKTLDPFETMLK-SLLRYQSGGGS
	 * * . * . * * *
	CP	DMECYKKYKGVWGFYDGRQPVLAITDPNMK-TVLVKECYSVFTNRRPFGPVGFMKNAIS
	HP	VSEN----HMRKKLYENGVTDSLKSNFALLKLSEELLDKWLSYPET-QHVPLSQHMLGF
10		. . * . . . * * * *
	CP	IAEDEEWKRIRSLSPFTTSGKLEMPPIAKYGDVLRNLRREAETGKPVTLKDVFGAY
	HP	AMKSVTQMVMG-----STF-EDDQEVIRFQKNHGTWVSEIGKGFLDGSLD--KNM
		. * . * . * * * *
	CP	SMDVITSTSFGVNIDSLNPNQDPFVENTKKLLRFDLDPFSLITIFPFIPILEVNLIS
15	HP	TRKKQYEDALMQ-LESVLRNIIKE-RKGR-NFSQHIF-----IDSLVQGNLNDQQILED
	 * * . * . * * *
	CP	IFPREVTSFLRKS VKRIKESRLKDTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQS
	HP	MIFSLASCIITAKLCTWAICFLTTS EEVQKKLYEEINQVF-GNGPVTPEKIEQLRYCQHV
		. * * . . . * * . * . . * . * . . * . * . . *
20	CP	IIFIFAGYETTSSVLSFIIYELATHPDVQKQLQEEIDTVLPNKAPPTYDTVLQMEYLDMV
	HP	LCETVRTAKLTPVSAQLQDIEGKIDRFIIPRETFLVLYALGVVLQDPNTWPSPHKFDPRF
		. * * * . . * * . * . * . * . * . *
	HP	VNETLRIFPIAMRLERVCKKDVEINGIFIPKGVVVMIPSYALHHPKYWPEPEKFLPERF
	HP	----DDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLSVEGQVIETKYE
25		. * * * . . . * * *
	CP	SKKNNDNIDPYIYTPFG-SGPRNCIGMRFALNMKLAIIRVLQNF SFKPCKETQIPLKLR
	HP	LVTSSREEAWITVSKRY
		*
	CP	LGGLLQTEKPIVLKIESRDGTVSGA

30

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs

possessing the homology of 90% or more (for example, Accession No. AA381169), but it can not be assessed whether these ESTs with partial sequences code for the same protein as the protein of the present invention.

- 5 The cytochrome P450 participates in the drug metabolism and can be utilized as a catalyst in organic synthesis reactions such as oxidation and so on.

<HP10419> (Sequence Number 12, 30, 48)

- 10 Determination of the whole base sequence for the cDNA insert of clone HP10419 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 170 bp, an ORF of 744 bp, and a 3'-non-translation region of 1116 bp. The ORF codes for a protein consisting of 247 amino acid residues with a hydrophobic region
15 of putative seven transmembrane domains. Figure 13 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method.

- 20 The search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. AA340663), but it can not be assessed whether these ESTs with partial sequences code for the same protein as the protein of the present invention.

<HP10424> (Sequence Number 13, 31, 49)

- 25 Determination of the whole base sequence for the cDNA insert of clone HP10424 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 97 bp, an ORF of 342 bp, and a 3'-non-translation region of 54 bp. The ORF codes for a protein

consisting of 113 amino acid residues with one transmembrane domain at the N-terminal. Figure 14 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that
5 the present protein remained in the membrane from the observation that the urokinase secretion was not identified upon transduction into the COS7 cells of an expression vector in which a HindIII-AccI fragment (after the Klenow treatment) containing a cDNA fragment encoding the N-terminal 58 amino
10 acid residues in the present protein was inserted at the HindIII-SmaI site of pSSD3. The in vitro translation resulted in the formation of a translation product of 14 kDa that was somewhat larger than the molecular weight of 12,784 predicted from the ORF.

15 Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. AA401979), but it can not be assessed whether these ESTs with partial sequences code for the same protein as the protein
20 of the present invention.

<HP10428> (Sequence Number 14, 32, 50)

Determination of the whole base sequence for the cDNA insert of clone HP10428 obtained from the human epidermoid carcinoma cell line KBc cDNA libraries revealed the structure
25 consisting of a 5'-non-translation region of 287 bp, an ORF of 1098 bp, and a 3'-non-translation region of 659 bp. The ORF codes for a protein consisting of 365 amino acid residues with a hydrophobic region of putative nine transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile of

the present protein obtained by the Kyte-Doolittle method. The result of the in vitro translation did not reveal the formation of distinct bands and only revealed the formation of smeary bands at the high-molecular-weight position.

5 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was analogous to the baker's yeast hypothetical membrane protein YML038c (NBRF Accession No. S49741). Table 13 indicates the comparison of the amino acid sequences between the human
10 protein of the present invention (HP) and the baker's yeast hypothetical membrane protein YML038c (SC). - represents a gap, * represents an amino acid residue identical to that in the protein of the present invention, and . represents an amino acid residue analogous to that in the protein of the present
15 invention. The both proteins possessed a homology of 26.3% among the N-terminal region of 281 amino acid residues.

Table 13

	HP	MGRWALDVAFLWKAVLTGLVL-LYYCFSIGITFYNKWL-----TKSFHFPFLFMTMLHLA
		*... *... *...*. *
5	SC	MNRTVFLAFVFGWYFCS-IALSIYNRMFDPKDLGIGYPVLVTTTFHQA
	HP	VIFLFSALSRAVQ---CSSHRARVLSWADYLRRVAPTALATALDVGLSNWSFLYVTVS
		...*. * . . * . . * . . * . . * . . * . . *
	SC	TLWLLSGIYIKLRHKPVKNVLRKNNGFNWSFFLKFLPTAVASAGDIGLSNVSFQYVPLT
	HP	LYTMTKSSAVLFILFSLIFKLEEL--RAALVLVVLLIAGGLFMF-----TYKSTQ-FN
10		.***.***. *...*. *****. . ** *...* . *...*
	SC	IYTIKSSSIAFVLLFGCIPKLEKFWKLALSVIIMFVGVALMVFKPSDSTSTKNDQALV
	HP	VEGFALVLGASFIGGIRWTLTQMLLQKAELGLQNPIDTMFHLQPLMFLGLFPLFAVFEGL
		. * *...* ..*... *****. *
	SC	IFGSFLVLASSCLSGLRWVYTQLMLRNNPIQTNTAAVEES-DGALFTENEDNVDNEPVV
15	HP	HLSTSEKIFRFQDT-GLLLRVLGSFLGGLAFGLGFSEFLVSRSSLTLSIAGIFKEV
		. * * * . *...* ... *...* . . * ...*
	SC	NLANNKMLENFGESKPHPIHTIHQ--LAPIMGITLLLS-LLVEKPFPGIFS-SSIFRLD
	HP	CTLLLAHLLGDQISLLNLGFGALCLSGISLHVALKALHSRGDGGPKALKGLGSSPDLEL
20	SC	TSNGGVGTETTIVLSIVRGIVLLILPGFAVFLLTICEFSILEQTPVLTVSIVGIVKELLTV
	HP	LLRSSQREEGDNEEEYFVAQGQQ
	SC	IFGIIILSERLSGFYNWLGMLIIMADVCIYNYFRYKQDLLQKYHSVSTQDNRNELKGFQD

Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. AA018345), but it can not be assessed whether these ESTs

with partial sequences code for the same protein as the protein of the present invention.

<HP10429> (Sequence Number 15, 33, 51)

Determination of the whole base sequence for the cDNA
5 insert of clone HP10429 obtained from the human stomach cancer
cDNA libraries revealed the structure consisting of a 5'-non-
translation region of 156 bp, an ORF of 681 bp, and a 3'-non-
translation region of 206 bp. The ORF codes for a protein
consisting of 226 amino acid residues with four transmembrane
10 domains. Figure 16 depicts the hydrophobicity/hydrophilicity
profile of the present protein obtained by the Kyte-Doolittle
method. The in vitro translation resulted in the formation of
a translation product of 25 kDa that was almost consistent with
the molecular weight of 25,321 predicted from the ORF.

15 The search of the protein data base using the amino acid
sequence of the present protein revealed that the protein was
not analogous to any known proteins. Furthermore, the search of
GenBank using the base sequence of the present cDNA revealed
that there existed some ESTs possessing the homology of 90% or
20 more (for example, Accession No. AA315933), but it can not be
assessed whether these ESTs with partial sequences code for the
same protein as the protein of the present invention.

<HP10432> (Sequence Number 16, 34, 52)

Determination of the whole base sequence for the cDNA
25 insert of clone HP10429 obtained from the human liver cDNA
libraries revealed the structure consisting of a 5'-non-
translation region of 28 bp, an ORF of 390 bp, and a 3'-non-
translation region of 554 bp. The ORF codes for a protein
consisting of 129 amino acid residues with a signal-like

sequence at the N-terminal and one interior transmembrane domain. Therefore, the present protein is considered to be a type-I membrane protein. Figure 17 depicts the hydrophobicity/hydrophilicity profile of the present protein
5 obtained by the Kyte-Doolittle method.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed
10 that there existed some ESTs possessing the homology of 90% or more (for example, Accession No. T74424), but the same ORF as that in the present cDNA was not identified.

<HP10433> (Sequence Number 17, 35, 53)

Determination of the whole base sequence for the cDNA
15 insert of clone HP10433 obtained from the human liver cDNA libraries revealed the structure consisting of a 5'-non-translation region of 72 bp, an ORF of 492 bp, and a 3'-non-translation region of 131 bp. The ORF codes for a protein consisting of 163 amino acid residues with one transmembrane
20 domain at the N-terminal. Figure 18 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. It was indicated that the present protein remained in the membrane from the observation that the urokinase secretion was not identified
25 upon transduction into the COS7 cells of an expression vector in which a HindIII-Eco81I fragment (treated with the mung-bean nuclease) containing a cDNA fragment encoding the N-terminal 137 amino acid residues in the present protein was inserted at the HindIII-EcoRV site of pSSD3. Therefore, the present protein

is considered to be a type-II membrane protein. The in vitro translation resulted in the formation of a translation product of 21 kDa that was almost consistent with the molecular weight of 18,617 predicted from the ORF.

5 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or
10 more (for example, Accession No. H84693), but many sequences are not distinct and the same ORF as that in the present cDNA was not identified.

<HP10480> (Sequence Number 18, 36, 54)

Determination of the whole base sequence for the cDNA
15 insert of clone HP10480 obtained from the human stomach cancer cDNA libraries revealed the structure consisting of a 5'-non-translation region of 79 bp, an ORF of 582 bp, and a 3'-non-translation region of 1253 bp. The ORF codes for a protein consisting of 193 amino acid residues with four transmembrane
20 domains. Figure 19 depicts the hydrophobicity/hydrophilicity profile of the present protein obtained by the Kyte-Doolittle method. The in vitro translation resulted in the formation of a translation product of 23 kDa that was somewhat larger than the molecular weight of 21,445 predicted from the ORF.

25 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was not analogous to any known proteins. Furthermore, the search of GenBank using the base sequence of the present cDNA revealed that there existed some ESTs possessing the homology of 90% or

more (for example, Accession No. W93606), but many sequences are not distinct and the same ORF as that in the present cDNA was not identified.

The present invention provides human proteins having
5 transmembrane domains and cDNAs encoding said proteins. All of the proteins of the present invention are putative proteins controlling the proliferation and differentiation of the cells, because said proteins exist on the cell membrane. Therefore, the proteins of the present invention can be used as
10 pharmaceuticals or as antigens for preparing antibodies against said proteins. Furthermore, said DNAs can be used for the expression of large amounts of said proteins. The cells expressing large amounts of membrane proteins with transfection of these membrane protein genes can be applied to the detection
15 of the corresponding ligands, the screening of novel low-molecular medicines, and so on.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological activities
20 (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies
25 or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for

analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as
5 molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA
10 sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for
15 examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in
20 a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

25 The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in

assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of
5 tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which
10 binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of
15 being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A
20 Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

25 Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source

and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation

10 Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

25 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H.

Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 5 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of 10 spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse 15 and human Interferon γ , Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without 20 limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 25 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 -Nordan, R. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et

- al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.
- 10 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in
- 15 Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans);
- 20 Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

- 25 A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined

immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be
5 caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis
10 viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

15 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis,
20 insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or
25 other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be

possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of 5 activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, 10 which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure 15 to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful 20 in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its 25 recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2

activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., *Science* 257:789-792 (1992) and Turka et al., *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease.

The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B

lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte
5 antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or
10 together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein
15 of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

20 In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least
25 one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression

vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression
5 of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface
10 of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II
15 molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins
20 on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which
25 blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a

T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 5 Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays
10 for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol.
15 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988;
20 Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

- Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that
25 affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John

Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those
5 described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in
10 Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that
15 activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine
20 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of
25 Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in:

Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently

of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation
5 of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal
10 nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells
15 or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

20 Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology
25 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney,

M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high
5 proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of
10 Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc.,
15 New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

20 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

25 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the

invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, 5 trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract 10 bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or 15 processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, 20 which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a 25 tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue

formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders,

such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

5 Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

10 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular
15 endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

20 A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for
25 promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of

the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

- 5 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale
10 et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or
15 chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell
20 population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of
25 infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell

population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A

protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses).

Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors

of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include
5 without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al.,
10 Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

15 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by
20 inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can
25 be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis,

complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be
5 useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of
10 the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary
15 to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth

20 Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi
25 and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in

bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, 5 protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent 10 behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related 15 diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another 20 material or entity which is cross-reactive with such protein.

Sequence Table

(2) INFORMATION FOR SEQ ID NO: 1:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

10 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

15 (D) CLONE NAME: HP01263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Gly Leu Leu Leu Pro Leu Ala Leu Cys Ile Leu Val Leu Cys Cys
 20 1 5 10 15
 Gly Ala Met Ser Pro Pro Gln Leu Ala Leu Asn Pro Ser Ala Leu Leu
 20 25 30
 Ser Arg Gly Cys Asn Asp Ser Asp Val Leu Ala Val Ala Gly Phe Ala
 35 40 45
 25 Leu Arg Asp Ile Asn Lys Asp Arg Lys Asp Gly Tyr Val Leu Arg Leu
 50 55 60
 Asn Arg Val Asn Asp Ala Gln Glu Tyr Arg Arg Gly Gly Leu Gly Ser
 65 70 75 80
 Leu Phe Tyr Leu Thr Leu Asp Val Leu Glu Thr Asp Cys His Val Leu
 30 85 90 95
 Arg Lys Lys Ala Trp Gln Asp Cys Gly Met Arg Ile Phe Phe Glu Ser
 100 105 110
 Val Tyr Gly Gln Cys Lys Ala Ile Phe Tyr Met Asn Asn Pro Ser Arg
 115 120 125
 35 Val Leu Tyr Leu Ala Ala Tyr Asn Cys Thr Leu Arg Pro Val Ser Lys
 130 135 140
 Lys Lys Ile Tyr Met Thr Cys Pro Asp Cys Pro Ser Ser Ile Pro Thr
 145 150 155 160

84

Asp Ser Ser Asn His Gln Val Leu Glu Ala Ala Thr Glu Ser Leu Ala
 165 170 175
 Lys Tyr Asn Asn Glu Asn Thr Ser Lys Gln Tyr Ser Leu Phe Lys Val
 180 185 190
 5 Thr Arg Ala Ser Ser Gln Trp Val Val Gly Pro Ser Tyr Phe Val Glu
 195 200 205
 Tyr Leu Ile Lys Glu Ser Pro Cys Thr Lys Ser Gln Ala Ser Ser Cys
 210 215 220
 Ser Leu Gln Ser Ser Asp Ser Val Pro Val Gly Leu Cys Lys Gly Ser
 10 225 230 235 240
 Leu Thr Arg Thr His Trp Glu Lys Phe Val Ser Val Thr Cys Asp Phe
 245 250 255
 Phe Glu Ser Gln Ala Pro Ala Thr Gly Ser Glu Asn Ser Ala Val Asn
 260 265 270
 15 Gln Lys Pro Thr Asn Leu Pro Lys Val Glu Glu Ser Gln Gln Lys Asn
 275 280 285
 Thr Pro Pro Thr Asp Ser Pro Ser Lys Ala Gly Pro Arg Gly Ser Val
 290 295 300
 Gln Tyr Leu Pro Asp Leu Asp Asp Lys Asn Ser Gln Glu Lys Gly Pro
 20 305 310 315 320
 Gln Glu Ala Phe Pro Val His Leu Asp Leu Thr Thr Asn Pro Gln Gly
 325 330 335
 Glu Thr Leu Asp Ile Ser Phe Leu Phe Leu Glu Pro Met Glu Glu Lys
 340 345 350
 25 Leu Val Val Leu Pro Phe Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys
 355 360 365
 Pro Gly Pro Ala Gln Asn Ala Ser Pro Leu Val Leu Pro Pro
 370 375 380

30

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317

(B) TYPE: Amino acid

35

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP01299

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

Met Trp Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His
  1             5             10             15
10 Trp Tyr Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val
    20             25             30
Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln
    35             40             45
Leu Asp Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys
15     50             55             60
Gly Ala Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val
    65             70             75             80
Thr Leu Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp
    85             90             95
20 Val Lys Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn
    100             105             110
Ala Gly Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu
    115             120             125
Asp Ser Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val
25     130             135             140
Thr Leu Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val
    145             150             155             160
Asn Val Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr
    165             170             175
30 Cys Val Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg
    180             185             190
Glu Ile Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr
    195             200             205
Phe Arg Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys
35     210             215             220
Gln Ser Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln
    225             230             235             240
Gln Tyr Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu Leu Asn

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86

245 250 255
 Cys Ser Thr Asn Leu Asn Leu Val Thr Asp Cys Met Glu His Ala Leu
 260 265 270
 Thr Ser Val His Pro Arg Thr Arg Tyr Ser Ala Gly Trp Asp Ala Lys
 5 275 280 285
 Phe Phe Phe Ile Pro Leu Ser Tyr Leu Pro Thr Ser Leu Ala Asp Tyr
 290 295 300
 Ile Leu Thr Arg Ser Trp Pro Lys Pro Ala Gln Ala Val
 305 310 315

10

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296
 15 (B) TYPE: Amino acid
 (D) TOPOLOGY: Linear
 (ii) SEQUENCE KIND: Protein
 (iii) HYPOTHETICAL: No

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Liver
 (D) CLONE NAME: HP01347

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ser Asp Ser Lys Glu Pro Arg Val Gln Gln Leu Gly Leu Leu Gly
 1 5 10 15
 Cys Leu Gly His Gly Ala Leu Val Leu Gln Leu Leu Ser Phe Met Leu
 30 20 25 30
 Leu Ala Gly Val Leu Val Ala Ile Leu Val Gln Val Ser Lys Val Pro
 35 40 45
 Ser Ser Leu Ser Gln Glu Gln Ser Glu Gln Asp Ala Ile Tyr Gln Asn
 50 55 60
 35 Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys
 65 70 75 80
 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly
 85 90 95

87

Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Il Tyr Gln Glu Leu Thr
 100 105 110
 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln
 115 120 125
 5 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu
 130 135 140
 Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu
 145 150 155 160
 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile
 10 165 170 175
 Tyr Gln Glu Leu Thr Glu Leu Lys Ala Ala Val Gly Glu Leu Pro Glu
 180 185 190
 Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala
 195 200 205
 15 Ala Val Gly Glu Leu Pro Asp Gln Ser Lys Gln Gln Gln Ile Tyr Gln
 210 215 220
 Glu Leu Thr Asp Leu Lys Thr Ala Phe Glu Arg Leu Cys Arg His Cys
 225 230 235 240
 Pro Lys Asp Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn
 20 245 250 255
 Ser Gln Arg Asn Trp His Asp Ser Val Thr Ala Cys Gln Glu Val Arg
 260 265 270
 Ala Gln Leu Val Val Ile Lys Thr Ala Glu Glu Gln Leu Pro Ala Val
 275 280 285
 25 Leu Glu Gln Trp Arg Thr Gln Gln
 290 295

(2) INFORMATION FOR SEQ ID NO: 4:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

35 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

88

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

5
 Met Cys Thr Gly Lys Cys Ala Arg Cys Val Gly Leu Ser Leu Ile Thr
 1 5 10 15
 Leu Cys Leu Val Cys Ile Val Ala Asn Ala Leu Leu Leu Val Pro Asn
 20 25 30
 10 Gly Glu Thr Ser Trp Thr Asn Thr Asn His Leu Ser Leu Gln Val Trp
 35 40 45
 Leu Met Gly Gly Phe Ile Gly Gly Gly Leu Met Val Leu Cys Pro Gly
 50 55 60
 Ile Ala Ala Val Arg Ala Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys
 15 65 70 75 80
 Cys Gly Asn Arg Cys Arg Met Leu Arg Ser Val Phe Ser Ser Ala Phe
 85 90 95
 Gly Val Leu Gly Ala Ile Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu
 100 105 110
 20 Arg Asn Gly Pro Arg Cys Leu Met Asn Gly Glu Trp Gly Tyr His Phe
 115 120 125
 Glu Asp Thr Ala Gly Ala Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg
 130 135 140
 Cys Glu Ala Pro Pro Arg Val Val Pro Trp Asn Val Thr Leu Phe Ser
 25 145 150 155 160
 Leu Leu Val Ala Ala Ser Cys Leu Glu Ile Val Leu Cys Gly Ile Gln
 165 170 175
 Leu Val Asn Ala Thr Ile Gly Val Phe Cys Gly Asp Cys Arg Lys Lys
 180 185 190
 30 Gln Asp Thr Pro His
 195

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 221
 (B) TYPE: Amino acid
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 (D) CLONE NAME: HP01526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

10 Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys Val
    1           5           10           15
Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg His
    20           25           30
Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe Leu
15           35           40           45
Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu Lys
    50           55           60
Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
    65           70           75           80
20 Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
    85           90           95
Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly Tyr
    100          105          110
Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
25           115          120          125
Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
    130          135          140
Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
    145          150          155          160
30 Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp Cys
    165          170          175
Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
    180          185          190
Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr
35           195          200          205
Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu Leu Gln Thr
    210          215          220

```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251

(B) TYPE: Amino acid

5

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

15

Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala Ile Thr Arg

1 5 10 15

Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys Leu Gly

20 25 30

20 Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala Phe Leu Tyr

35 40 45

Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr Phe Pro Val

50 55 60

Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr Phe Leu Tyr

25 65 70 75 80

Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly Arg Pro Ala

85 90 95

Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile Val Ile Thr

100 105 110

30 Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu Ile Met Ser

115 120 125

Val Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile Val Ser Phe

130 135 140

Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu

35 145 150 155 160

Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly

165 170 175

Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met

91

180 185 190
 Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe Leu Tyr Arg
 195 200 205
 Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly Val Pro Pro
 5 210 215 220
 Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly Gly Arg His
 225 230 235 240
 Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln
 245 250

10

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106
 15 (B) TYPE: Amino acid
 (D) TOPOLOGY: Linear
 (ii) SEQUENCE KIND: Protein
 (iii) HYPOTHETICAL: No

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Epidermoid carcinoma
 (C) CELL LINE: KB
 (D) CLONE NAME: HP10389

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro Ser
 1 5 10 15
 30 Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn Pro
 20 25 30
 Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro Val
 35 40 45
 Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly Leu
 35 50 55 60
 Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met Arg
 65 70 75 80
 Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu Gly

92

85 90 95
 Leu Ala Val Thr Ala Met Lys Ser Arg Pro
 100 105

5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78
 10 (B) TYPE: Amino acid
 (D) TOPOLOGY: Linear
 (ii) SEQUENCE KIND: Protein
 (iii) HYPOTHETICAL: No

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 (D) CLONE NAME: HP10408

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly Ser
 1 5 10 15
 Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys Glu
 25 20 25 30
 Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu Glu Leu Leu
 35 40 45
 Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr
 50 55 60
 30 Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 9:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314
 (B) TYPE: Amino acid
 (D) TOPOLOGY: Linear

93

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 (D) CLONE NAME: HP10412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

10

Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly
 1 5 10 15
 Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
 20 25 30
 15 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala
 35 40 45
 Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro
 50 55 60
 Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala
 20 65 70 75 80
 Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val
 85 90 95
 Ile Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His
 100 105 110
 25 Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys
 115 120 125
 Gln Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu
 130 135 140
 Arg Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu
 30 145 150 155 160
 Glu Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys
 165 170 175
 Ala Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu
 180 185 190
 35 Lys Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr
 195 200 205
 Glu Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys
 210 215 220

94

Gln Ser Lys Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu
 225 230 235 240
 Arg Thr Gln Asp Thr Ile Asn Arg Ile Gln Asp Leu Leu Ala Glu Gly
 245 250 255
 5 Thr Ile Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile Tyr Ile Thr
 260 265 270
 Pro Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg Gln Arg Gly Arg
 275 280 285
 Val Ser Ile Ala Glu Leu Ala Gln Ala Ser Asn Ser Leu Ile Ala Trp
 10 290 295 300
 Gly Arg Glu Ser Pro Ala Gln Ala Pro Ala
 305 310

15 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

20 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

30 Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu
 1 5 10 15
 Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu
 20 25 30
 Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly
 35 35 40 45
 Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp Asp Glu Pro Pro Pro
 50 55 60
 Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg

95

65 70 75 80
 Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met Ala Ile Asn Gly Lys
 85 90 95
 Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr Gly Pro Glu Gly Pro
 5 100 105 110
 Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg Gly Leu Ala Thr Phe
 115 120 125
 Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr Asp Asp Leu Ser Asp
 130 135 140
 10 Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp Trp Glu Ser Gln Phe
 145 150 155 160
 Thr Phe Lys Tyr His His Val Gly Lys Leu Leu Lys Glu Gly Glu Glu
 165 170 175
 Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys Asp Glu Ser Ala Arg
 15 180 185 190
 Lys Asn Asp
 195

20 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

25 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

30 (B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

35 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val
 1 5 10 15
 Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile
 20 25 30

96

Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn L u Pro Asp Il
 35 40 45
 Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu His Glu Arg
 50 55 60
 5 Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser
 65 70 75 80
 Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro Asn Lys Thr
 85 90 95
 Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg Tyr Gln Ser
 10 100 105 110
 Gly Gly Gly Ser Val Ser Glu Asn His Met Arg Lys Lys Leu Tyr Glu
 115 120 125
 Asn Gly Val Thr Asp Ser Leu Lys Ser Asn Phe Ala Leu Leu Leu Lys
 130 135 140
 15 Leu Ser Glu Glu Leu Leu Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln
 145 150 155 160
 His Val Pro Leu Ser Gln His Met Leu Gly Phe Ala Met Lys Ser Val
 165 170 175
 Thr Gln Met Val Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile
 20 180 185 190
 Arg Phe Gln Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly
 195 200 205
 Phe Leu Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr
 210 215 220
 25 Glu Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys
 225 230 235 240
 Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser Leu
 245 250 255
 Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser Met Ile
 30 260 265 270
 Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys Thr Trp Ala
 275 280 285
 Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys Lys Leu Tyr Glu
 290 295 300
 35 Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val Thr Pro Glu Lys Ile
 305 310 315 320
 Glu Gln Leu Arg Tyr Cys Gln His Val Leu Cys Glu Thr Val Arg Thr
 325 330 335

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Ala Lys Leu Thr Pro Val Ser Ala Gln Leu Gln Asp Ile Glu Gly Lys
 340 345 350
 Ile Asp Arg Phe Ile Ile Pro Arg Glu Thr Leu Val Leu Tyr Ala Leu
 355 360 365
 5 Gly Val Val Leu Gln Asp Pro Asn Thr Trp Pro Ser Pro His Lys Phe
 370 375 380
 Asp Pro Asp Arg Phe Asp Asp Glu Leu Val Met Lys Thr Phe Ser Ser
 385 390 395 400
 Leu Gly Phe Ser Gly Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr
 10 405 410 415
 Met Val Thr Thr Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu
 420 425 430
 Leu Ser Val Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr
 435 440 445
 15 Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 450 455 460

(2) INFORMATION FOR SEQ ID NO: 12:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

25 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

30 (D) CLONE NAME: HP10419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro
 35 1 5 10 15
 Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val
 20 25 30
 Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu

98

35 40 45
 Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp
 50 55 60
 Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val
 5 65 70 75 80
 Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys
 85 90 95
 Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile
 100 105 110
 10 Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile
 115 120 125
 Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro
 130 135 140
 Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser
 15 145 150 155 160
 Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val
 165 170 175
 Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu Gly Leu
 180 185 190
 20 Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro
 195 200 205
 Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met
 210 215 220
 Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln
 25 225 230 235 240
 Arg Ser Leu Leu Cys Lys Asp
 245

30 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

35 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

99

(A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 (D) CLONE NAME: HP10424

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
 1 5 10 15
 Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
 10 20 25 30
 Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
 35 40 45
 Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
 50 55 60
 15 Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
 65 70 75 80
 Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
 85 90 95
 Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser
 20 100 105 110
 Thr

(2) INFORMATION FOR SEQ ID NO: 14:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365
 (B) TYPE: Amino acid
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

30 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Epidermoid carcinoma
 (C) CELL LINE: KB
 (D) CLONE NAME: HP10428

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

100

Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu
 1 5 10 15
 Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr
 20 25 30
 5 Phe Tyr Asn Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met
 35 40 45
 Thr Met Leu His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser Arg
 50 55 60
 Ala Leu Val Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser Trp
 10 65 70 75 80
 Ala Asp Tyr Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala Leu
 85 90 95
 Asp Val Gly Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser Leu
 100 105 110
 15 Tyr Thr Met Thr Lys Ser Ser Ala Val Leu Phe Ile Leu Ile Phe Ser
 115 120 125
 Leu Ile Phe Lys Leu Glu Glu Leu Arg Ala Ala Leu Val Leu Val Val
 130 135 140
 Leu Leu Ile Ala Gly Gly Leu Phe Met Phe Thr Tyr Lys Ser Thr Gln
 20 145 150 155 160
 Phe Asn Val Glu Gly Phe Ala Leu Val Leu Gly Ala Ser Phe Ile Gly
 165 170 175
 Gly Ile Arg Trp Thr Leu Thr Gln Met Leu Leu Gln Lys Ala Glu Leu
 180 185 190
 25 Gly Leu Gln Asn Pro Ile Asp Thr Met Phe His Leu Gln Pro Leu Met
 195 200 205
 Phe Leu Gly Leu Phe Pro Leu Phe Ala Val Phe Glu Gly Leu His Leu
 210 215 220
 Ser Thr Ser Glu Lys Ile Phe Arg Phe Gln Asp Thr Gly Leu Leu Leu
 30 225 230 235 240
 Arg Val Leu Gly Ser Leu Phe Leu Gly Gly Ile Leu Ala Phe Gly Leu
 245 250 255
 Gly Phe Ser Glu Phe Leu Leu Val Ser Arg Thr Ser Ser Leu Thr Leu
 260 265 270
 35 Ser Ile Ala Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala
 275 280 285
 His Leu Leu Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala
 290 295 300

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Leu Cys Leu Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His
 305 310 315 320
 Ser Arg Gly Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser
 325 330 335
 5 Pro Asp Leu Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp
 340 345 350
 Asn Glu Glu Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln
 355 360 365

10

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226

(B) TYPE: Amino acid

15

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

25

Met Pro Thr Thr Lys Lys Thr Leu Met Phe Leu Ser Ser Phe Phe Thr
 1 5 10 15
 Ser Leu Gly Ser Phe Ile Val Ile Cys Ser Ile Leu Gly Thr Gln Ala
 20 25 30
 30 Trp Ile Thr Ser Thr Ile Ala Val Arg Asp Ser Ala Ser Asn Gly Ser
 35 40 45
 Ile Phe Ile Thr Tyr Gly Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu
 50 55 60
 Ser His Gly Leu Ala Glu Pro Lys Lys Lys Phe Ala Val Leu Glu Ile
 35 65 70 75 80
 Leu Asn Asn Ser Ser Gln Lys Thr Leu His Ser Val Thr Ile Leu Phe
 85 90 95
 Leu Val Leu Ser Leu Ile Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe

102

100 105 110
 Tyr Asn Ser Ile Ser Asn Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly
 115 120 125
 Val Tyr Thr Trp Asn Gly Leu Gly Ala Ser Phe Val Phe Val Thr Met
 5 130 135 140
 Ile Leu Phe Val Ala Asn Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu
 145 150 155 160
 Phe Gln Met Leu Tyr Pro Ala Thr Thr Ser Lys Gly Thr Thr His Ser
 165 170 175
 10 Tyr Gly Tyr Ser Phe Trp Leu Ile Leu Leu Val Ile Leu Leu Asn Ile
 180 185 190
 Val Thr Val Thr Ile Ile Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg
 195 200 205
 Lys Gln Glu Gln Arg Lys Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile
 15 210 215 220
 Leu Phe
 225

20 (2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

25 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

30 (B) CELL KIND: Liver

(D) CLONE NAME: HP10432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

35 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
 1 5 10 15
 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
 20 25 30

103

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 Cys M t Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 5 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
 65 70 75 80
 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
 85 90 95
 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
 10 100 105 110
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
 115 120 125
 Gln

15

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163

20 (B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP10433

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly Ala Val Gly
 1 5 10 15
 Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly Leu Gln Val
 35 20 25 30
 Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp Ala Phe Gln
 35 40 45
 Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro Ala Gly Ile

104

50 55 60
 Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys Arg Lys Arg
 65 70 75 80
 Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly Arg Lys Arg
 5 85 90 95
 Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys Val Leu Gly
 100 105 110
 Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg Glu Ala Glu
 115 120 125
 10 Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala Gly Glu Asp
 130 135 140
 Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser Lys Ala Leu
 145 150 155 160
 Pro Arg Ser
 15

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 193
 (B) TYPE: Amino acid
 (D) TOPOLOGY: Linear
 (ii) SEQUENCE KIND: Protein
 (iii) HYPOTHETICAL: No

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 (D) CLONE NAME: HP10480

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
 1 5 10 15
 Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
 35 20 25 30
 Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
 35 40 45
 Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly

105

50 55 60
 Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Met
 65 70 75 80
 Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe
 5 85 90 95
 Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
 100 105 110
 Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile
 115 120 125
 10 Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Arg Ala
 130 135 140
 Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
 145 150 155 160
 Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
 15 165 170 175
 Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser
 180 185 190
 Ala

20

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146

(B) TYPE: Nucleic acid

25

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Linear

(D) CLONE NAME: HP01263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

35

ATGGGTCTGC TCCTTCCCT GGCACCTCTGC ATCCTAGTCC TGTGCTGCGG AGCAATGTCT 60
 CCACCCAGC TGGCCCTCAA CCCCTCGGCT CTGCTCTCCC GGGGCTGCAA TGA CTCCGAT 120
 GTGCTGGCAG TTGCAGGCTT TGCCCTGCGG GATATTAACA AAGACAGAAA GGATGGCTAT 180

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GTGCTGAGAC TCAACCGAGT GAACGACGCC CAGGAATACA GACGGGGTGG CCTGGGATCT 240
 CTGTTCTATC TTACTGGA TGTGCTAGAG ACTGACTGCC ATGTGCTCAG AAAGAAGGCA 300
 TGGCAAGACT GTGGAATGAG GATATTTTTT GAATCAGTTT ATGGTCAATG CAAAGCAATA 360
 TTTTATATGA ACAACCCAAG TAGAGTTCTC TATTTAGCTG CTTATAACTG TACTCTTCGC 420
 5 CCAGTTTCAA AAAAAAAGAT TTACATGACG TGCCCTGACT GCCCAAGCTC CATACCCACT 480
 GACTCTTCCA ATCACCAAGT GCTGGAGGCT GCCACCGAGT CTCTTGCGAA ATACAACAAT 540
 GAGAACACAT CCAAGCAGTA TTCTCTCTTC AAAGTCACCA GGGCTTCTAG CCAGTGGGTG 600
 GTCGGCCCTT CTTACTTTGT GGAATACTTA ATTAAAGAAT CACCATGTAC TAAATCCCAG 660
 GCCAGCAGCT GTTCACTTCA GTCCTCCGAC TCTGTGCCTG TTGGTCTTTG CAAAGGTTCT 720
 10 CTGACTCGAA CACTGCGGA AAAGTTTGTC TCTGTGACTT GTGACTTCTT TGAATCACAG 780
 GCTCCAGCCA CTGGAAGTGA AAAGTCTGCT GTTAACCAGA AACCTACAAA CCTTCCCAAG 840
 GTGGAAGAAT CCCAGCAGAA AAACACCCCC CCAACAGACT CCCCCTCAA AGCTGGGCCA 900
 AGAGGATCTG TCCAATATCT TCCTGACTTG GATGATAAAA ATTCCCAGGA AAAGGGCCCT 960
 CAGGAGGCCT TTCCTGTGCA TCTGGACCTA ACCACGAATC CCCAGGGAGA AACCTGGAT 1020
 15 ATTTCTTCC TCTTCCTGGA GCCTATGGAG GAGAAGCTGG TTGTCCTGCC TTTCCCCAAA 1080
 GAAAAAGCAC GCACTGCTGA GTGCCCAGGG CCAGCCCAGA ATGCCAGCCC TCTTGTCTT 1140
 CCGCCA 1146

20 (2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 951

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

30 (B) CELL KIND: Liver

(D) CLONE NAME: HP01299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

35 ATGTGGCTCT ACCTGGCGGC CTTGCTGGGC CTGTACTACC TTCTGCACTG GTACCGGGAG 60
 AGGCAGGTGG TGAGCCACCT CCAAGACAAG TATGTCTTTA TCACGGGCTG TGAAGCGGGC 120
 TTTGGGAACC TGCTGGCCAG ACAGCTGGAT GCACGAGGCT TGAGAGTGCT GGCTGCGTGT 180
 CTGACGGAGA AGGGGGCCGA GCAGCTGAGG GGCCAGACGT CTGACAGGCT GGAGACGGTG 240

107

ACCCTGGATG TTACCAAGAT GGAGAGCATC GCTGCAGCTA CTCAGTGGGT GAAGGAGCAT 300
 GTGGGGGACA GAGGACTCTG GGGACTGGTG AACCAATGCAG GCATTCTTAC ACCAATTACC 360
 TTATGTGAGT GGCTGAACAC TGAGGACTCT ATGAATATGC TCAAAGTGAA CCTCATTGGT 420
 GTGATCCAGG TGACCTTGAG CATGCTTCCT TTGGTGAGGA GAGCACGGGG AAGAATTGTC 480
 5 AATGTCTCCA GCATTCTGGG AAGAGTTGCT TTCTTTGTAG GAGGCTACTG TGTCTCCAAG 540
 TATGGAGTGG AAGCCTTTTC AGATATTCTG AGGCGTGAGA TTCAACATTT TGGGGTGAAA 600
 ATCAGCATAG TTGAACCTGG CTACTTCAGA ACGGGAATGA CAAACATGAC ACAGTCCTTA 660
 GAGCGAATGA AGCAAAGTTG GAAAGAAGCC CCCAAGCATA TTAAGGAGAC CTATGGACAG 720
 CAGTATTTTG ATGCCCTTTA CAATATCATG AAGGAAGGGC TGTGAATTG TAGCACAAAC 780
 10 CTGAACCTGG TCACTGACTG CATGGAACAT GCTCTGACAT CGGTGCATCC GCGAACTCGA 840
 TATTCAGCTG GCTGGGATGC TAAATTTTTC TTCATCCCTC TATCTTATTT ACCTACATCA 900
 CTGGCAGACT ACATTTTGAC TAGATCTTGG CCCAAACCAG CCCAGGCAGT C 951

15 (2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP01347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

30 ATGAGTGA CT CCAAGGAACC AAGGGTGCAG CAGCTGGGCC TCCTGGGGTG TCTTGCCCAT 60
 GGCGCCCTGG TGCTGCAACT CCTCTCCTTC ATGCTCTTGG CTGGGGTCCT GGTGGCCATC 120
 CTTGTCCAAG TGTCCAAGGT CCCAGCTCC CTAAGTCAGG AACCAATCCGA GCAAGACGCA 180
 ATCTACCAGA ACCTGACCCA GCTTAAAGCT GCAGTGGGTG AGCTCTCAGA GAAATCCAAG 240
 CTGCAGGAGA TCTACCAGGA GCTGACCCAG CTGAAGGCTG CAGTGGGTGA GTTGCCAGAG 300
 35 AAATCCAAGC TGCAGGAGAT CTACCAGGAG CTGACCCGGC TGAAGGCTGC AGTGGGTGAG 360
 TTGCCAGAGA AATCCAAGCT GCAGGAGATC TACCAGGAGC TGACCCGGCT GAAGGCTGCA 420
 GTGGGTGAGT TGCCAGAGAA ATCCAAGCTG CAGGAGATCT ACCAGGAGCT GACCCGGCTG 480
 AAGGCTGCAG TGGGTGAGTT GCCAGAGAAA TCCAAGCTGC AGGAGATCTA CCAGGAGCTG 540

108

ACGGAGCTGA AGGCTGCAGT GGGTGAGTTG CCAGAGAAAT CCAAGCTGCA GGAGATCTAC 600
 CAGGAGCTGA CCCAGCTGAA GGCTGCAGTG GGTGAGTTGC CAGACCAGTC CAAGCAGCAG 660
 CAAATCTATC AAGAACTGAC CGATTGGAAG ACTGCATTG AACGCCTGTG CCGCCACTGT 720
 CCCAAGGACT GGACATTCTT CCAAGGAAAC TGTTACTTCA TGTCTAACTC CCAGCGGAAC 780
 5 TGGCAGGACT CCGTCACCGC CTGCCAGGAA GTGAGGGCCC AGCTCGTCGT AATCAAAACT 840
 GCTGAGGAGC AGCTCCAGC GGTACTGGAA CAGTGGAGAA CCCAACAA 888

(2) INFORMATION FOR SEQ ID NO: 22:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 20 (D) CLONE NAME: HP01440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ATGTGTACGG GAAAATGTGC CCGCTGTGTG GGGCTCTCCC TCATTACCCT CTGCCTCGTC 60
 25 TGCATTGTGG CCAACGCCCT CCTGCTGGTA CCTAATGGGG AGACCTCCTG GACCAACACC 120
 AACCATCTCA GCTTGCAAGT CTGGCTCATG GGCGGCTTCA TTGGCGGGGG CCTAATGGTA 180
 CTGTGTCCGG GGATTGCAGC CGTTCGGGCA GGGGGCAAGG GCTGCTGTGG TGCTGGGTGC 240
 TGTGGAACC GCTGCAGGAT GCTGCGCTCG GTCTTCTCCT CGGCGTTCGG GGTGCTTGGT 300
 GCCATCTACT GCCTCTCGGT GTCTGGAGCT GGGCTCCGAA ATGGACCCAG ATGCTTAATG 360
 30 AACGGCGAGT GGGGCTACCA CTTGGAAGAC ACCGCGGGAG CTTACTTGCT CAACCGCACT 420
 CTATGGGATC GGTGCGAGGC GCCCCCTCGC GTGGTCCCCT GGAATGTGAC GCTCTTCTCG 480
 CTGCTGGTGG CCGCCTCCTG CCTGGAGATA GTACTGTGTG GGATCCAGCT GGTGAACGCG 540
 ACCATTGGTG TCTTCTGCGG CGATTGCAGG AAAAAACAGG ACACCCCTCA C 591

35

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663

109

- (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
(ii) SEQUENCE KIND: cDNA to mRNA

5

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Homo sapiens*
(B) CELL KIND: Stomach cancer
(D) CLONE NAME: HP01526

10

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATGGAGGCGG GCGGCTTTCT GGA CTGCTC ATTTACGGAG CATGCGTGGT CTTCA CCCTT 60
GGCATGTTCT CCGCCGGCCT CTCGGACCTC AGGCACATGC GAATGACCCG GAGTGTGGAC 120
15 AACGTCCAGT TCCTGCCCTT TCTCACCACG GAAGTCAACA ACCTGGGCTG GCTGAGTTAT 180
GGGGCTTTGA AGGGAGACGG GATCCTCATC GTCGTCAACA CAGTGGGTGC TGGCCTTCAG 240
ACCCTGTATA TCTTGGCATA TCTGCATTAC TGCCCTCGGA AGCGTGTTGT GCTCCTACAG 300
ACTGCAACCC TGCTAGGGGT CCTTCTCCTG GGTATGGCT ACTTTTGGCT CCTGGTACCC 360
AACCCTGAGG CCCGGCTTCA GCAGTTGGGC CTCTTCTGCA GTGTCTTCAC CATCAGCATG 420
20 TACCTCTCAC CACTGGCTGA CTTGGCTAAG GTGATTCAAA CTAAATCAAC CCAATGTCTC 480
TCCTACCCAC TCACCATTGC TACCCTTCTC ACCTCTGCCT CCTGGTGCCT CTATGGGTTT 540
CGACTCAGAG ATCCCTATAT CATGGTGTCC AACTTTCCAG GAATCGTCAC CAGCTTTATC 600
CGCTTCTGGC TTTTCTGGAA GTACCCCCAG GAGCAAGACA GGA ACTACTG GCTCCTGCAA 660
ACC 663

25

- (2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

30

- (ii) SEQUENCE KIND: cDNA to mRNA

35

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Homo sapiens*
(B) CELL KIND: Stomach cancer
(D) CLONE NAME: HP10230

110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

ATGTCGGACA TCGGAGACTG GTTCAGGAGC ATCCCGGCGA TCACGCGCTA TTGGTTCGCC      60
GCCACCGTCG CCGTGCCCTT GGTCGGCAAA CTCGGCCTCA TCAGCCCGGC CTACCTCTTC      120
5  CTCTGGCCCC AAGCCTTCCT TTATCGCTTT CAGATTGGA GGCCAATCAC TGCCACCTTT      180
TATTTCCCTG TGGGTCCAGG AACTGGATTT CTTTATTGG TCAATTTATA TTTCTTATAT      240
CAGTATTCTA CGCGACTTGA AACAGGAGCT TTTGATGGGA GGCCAGCAGA CTATTTATTC      300
ATGCTCCTCT TTAAGTGGAT TTGCATCGTG ATTACTGGCT TAGCAATGGA TATGCAGTTG      360
CTGATGATTC CTCTGATCAT GTCAGTACTT TATGTCTGGG CCCAGCTGAA CAGAGACATG      420
10 ATTGTATCAT TTTGGTTTGG AACACGATTT AAGGCCTGCT ATTTACCCTG GGTTATCCTT      480
GGATTCAACT ATATCATCGG AGGCTCGGTA ATCAATGAGC TTATTGAAA TCTGGTTGGA      540
CATCTTTATT TTTTCCTAAT GTTCAGATAC CCAATGGACT TGGGAGGAAG AAATTTTCTA      600
TCCACACCTC AGTTTTTGTA CCGCTGGCTG CCCAGTAGGA GAGGAGGAGT ATCAGGATTT      660
GGTGTGCCCC CTGCTAGCAT GAGGCGAGCT GCTGATCAGA ATGGCGGAGG CGGGAGACAC      720
15 AACTGGGGCC AGGGCTTTTC ACTTGGAGAC CAG                                     753

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(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 318
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

(ii) SEQUENCE KIND: cDNA to mRNA

25

(vi) ORIGINAL SOURCE:

```

      (A) ORGANISM: Homo sapiens
      (B) CELL KIND: Epidermoid carcinoma
      (C) CELL LINE: KB
30  (D) CLONE NAME: HP10389

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

ATGGCGACTC CCGGCCCTGT GATTCCGGAG GTCCCTTTG AACCATCGAA GCCTCCAGTC      60
35 ATTGAGGGGC TGAGCCCCAC TGTTTACAGG AATCCAGAGA GTTCAAGGA AAAGTTCGTT      120
CGCAAGACCC GCGAGAACCC GGTGGTACCC ATAGGTTGCC TGGCCACGGC GGCCGCCCTC      180
ACCTACGGCC TCTACTCCTT CCACCGGGGC AACAGCCAGC GCTCTCAGCT CATGATGCGC      240
ACCCGGATCG CCGCCAGGG TTTACGGTC GCAGCCATCT TGCTGGGTCT GGCTGTCACT      300

```


111

GCTATGAAGT CTCGACCC

318

(2) INFORMATION FOR SEQ ID NO: 26:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

10 (ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

15 (D) CLONE NAME: HP10408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

	ATGGGGTCTG GGCTGCCCCCT TGTCTCCTC TTGACCTCC TTGGCAGCTC ACATGGAACA	60
20	GGGCCGGGTA TGACTTTGCA ACTGAAGCTG AAGGAGTCTT TTCTGACAAA TTCCTCCTAT	120
	GAGTCCAGCT TCCTGGAATT GCTTGAAAAG CTCTGCCTCC TCCTCCATCT CCCTTCAGGG	180
	ACCAGCGTCA CCCTCCACCA TGCAAGATCT CAACACCATG TTGTCTGCAA CACA	234

25 (2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 942

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

35 (B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

112

ATGGTGGCGC CTGTGTGGTA CTTGGTAGCG GCGGCTCTGC TAGTCGGCTT TATCCTCTTC 60
 CTGACTCGCA GCCGGGGCCG GCGGCATCA GCCGGCCAAG AGCCACTGCA CAATGAGGAG 120
 CTGGCAGGAG CAGGCCGGGT GGCCACGCT GGGCCCTGG AGCCTGAGGA GCCGAGAGCT 180
 GGAGGCAGGC CTCGGCGCCG GAGGGACCTG GGCAGCCGCC TACAGGCCCA GCGTCGAGCC 240
 5 CAGCGGGTGG CCTGGGCAGA AGCAGATGAG AACGAGGAGG AAGCTGTCAT CCTAGCCCAG 300
 GAGGAGGAAG GTGTCGAGAA GCCAGCGGAA ACTCACCTGT CGGGGAAAAT TGGAGCTAAG 360
 AAACTGCGGA AGCTGGAGGA GAAACAAGCG CGAAAGGCC AGCGTGAGGC AGAGGAGGCT 420
 GAACGTGAGG AGCGGAAACG ACTCGAGTCC CAGCGCGAAG CTGAGTGGA GAAGGAGGAG 480
 GAGCGGCTTC GCCTGGAGGA GGAGCAGAAG GAGGAGGAGG AGAGGAAGGC CCGCGAGGAG 540
 10 CAGGCCACG GGGAGCATGA GGAGTACCTG AAACTGAAGG AGGCCTTTGT GGTGGAGGAG 600
 GAAGGCGTAG GAGAGACCAT GACTGAGGAA CAGTCCCAGA GCTTCCTGAC AGAGTTCATC 660
 AACTACATCA AGCAGTCCAA GGTGTGCTC TTGGAAGACC TGGCTTCCCA GGTGGGCCTA 720
 CGCACTCAGG ACACCATAAA TCGCATCCAG GACCTGCTGG CTGAGGGGAC TATAACAGGT 780
 GTGATTGACG ACCGGGGCAA GTTCATCTAC ATAACCCAG AGGAACTGGC CGCCGTGGCC 840
 15 AACTTCATCC GACAGCGGG CCGGGTGTCC ATCGCCGAGC TTGCCCAAGC CAGCAACTCC 900
 CTCATCGCCT GGGGCCGGGA GTCCCCTGCC CAAGCCCCAG CC 942

(2) INFORMATION FOR SEQ ID NO: 28:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25 (ii) SEQUENCE KIND: cDNA to mRNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 30 (D) CLONE NAME: HP10413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ATGGCTGCCG AGGATGTGGT GGCGACTGGC GCCGACCCAA GCGATCTGGA GAGCGGCGGG 60
 35 CTGCTGCATG AGATTTTCAC GTCGCCGCTC AACCTGCTGC TGCTTGGCCT CTGCATCTTC 120
 CTGCTCTACA AGATCGTGCG CGGGGACCAG CCGGCGGCCA GCGGCGACAG CGACGACGAC 180
 GAGCCGCCCC CTCTGCCCCG CCTCAAGCGG CGCGACTTCA CCCCCGCCGA GCTGCGGCGC 240
 TTCGACGGCG TCCAGGACCC GCGCATACTC ATGGCCATCA ACGGCAAGGT GTTCGATGTG 300

113

ACCAAAGGCC GCAAATTCTA CGGGCCCCGAG GGGCCGTATG GGGTCTTTGC TGGAAGAGAT 360
GCATCCAGGG GCCTTGCCAC ATTTTGCCTG GATAAGGAAG CACTGAAGGA TGAGTACGAT 420
GACCTTTCTG ACCTCACTGC TGCCCAGCAG GAGACTCTGA GTGACTGGGA GTCTCAGTTC 480
ACTTTCAAGT ATCATCACGT GGGCAAACCTG CTGAAGGAGG GGGAGGAGCC CACTGTGTAC 540
5 TCAGATGAGG AAGAACCAAA AGATGAGAGT GCCCGGAAAA ATGAT 585

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1386

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10415

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ATGTTGGA CT TCGCGATCTT CGCCGTTACC TTCTTGCTGG CGTTGGTGGG AGCCGTGCTC 60
TACCTCTATC CGGCTTCCAG ACAAGCTGCA GGAATTCCAG GGATTACTCC AACTGAAGAA 120
25 AAAGATGGTA ATCTTCCAGA TATTGTGAAT AGTGGAAGTT TGCATGAGTT CCTGGTTAAT 180
TTGCATGAGA GATATGGGCC TGTGGTCTCC TTCTGGTTTG GCAGGCGCCT CGTGGTTAGT 240
TTGGGCACTG TTGATGTACT GAAGCAGCAT ATCAATCCCA ATAAGACATT GGACCCTTTT 300
GAAACCATGC TGAAGTCATT ATTAAGGTAT CAATCTGGTG GTGGCAGTGT GAGTGAAAAC 360
CACATGAGGA AAAAATTGTA TGAAAATGGT GTGACTGATT CTCTGAAGAG TAACTTTGCC 420
30 CTCCTCCTAA AGCTTTTCAGA AGAATTATTA GATAAATGGC TCTCCTACCC AGAGACCCAG 480
CACGTGCCCC TCAGCCAGCA TATGCTTGGT TTTGCTATGA AGTCTGTTAC ACAGATGGTA 540
ATGGGTAGTA CATTTGAAGA TGATCAGGAA GTCATTGCT TCCAGAAGAA TCATGGCACA 600
GTTTGGTCTG AGATTGAAA AGGCTTTCTA GATGGGTCAC TTGATAAAAA CATGACTCGG 660
AAAAACAAT ATGAAGATGC CCTCATGCAA CTGGAGTCTG TTTTAAGGAA CATCATAAAA 720
35 GAACGAAAAG GAAGGAACCT CAGTCAACAT ATTTTCATTG ACTCCTTAGT ACAAGGGAAC 780
CTTAATGACC AACAGATCCT AGAAGACAGT ATGATATTTT CTCTGGCCAG TTGCATAATA 840
ACTGCAAAAT TGTGTACCTG GGCAATCTGT TTTTAAACCA CCTCTGAAGA AGTTCAAAAA 900
AAATTATATG AAGAGATAAA CCAAGTTTTT GGAAATGGTC CTGTTACTCC AGAGAAAATT 960

114

GAGCAGCTCA GATATTGTCA GCATGTGCTT TGTGAACTG TTCGAACTGC CAAACTGACT 1020
 CCAGTTTCTG CCCAGCTTCA AGATATTGAA GGAAAAATTG ACCGATTTAT TATTCCTAGA 1080
 GAGACCCTCG TCCTTTATGC CCTTGGTGTG GTACTTCAGG ATCCTAATAC TTGGCCATCT 1140
 CCACACAAGT TTGATCCAGA TCGGTTTGAT GATGAATTAG TAATGAAAAC TTTTTCCTCA 1200
 5 CTTGGATTCT CAGGCACACA GGAGTGCCA GAGTTGAGGT TTGCATATAT GGTGACCACA 1260
 GTACTTCTTA GTGTATTGGT GAAGAGACTG CACCTACTTT CTGTGGAGGG ACAGGTTATT 1320
 GAAACAAAGT ATGAACTGGT AACATCATCA AGGAAGAAG CTTGGATCAC TGTCTCAAAG 1380
 AGATAT 1386

10

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741

(B) TYPE: Nucleic acid

15

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

25

ATGGGGGCTG CGGTGTTTTT CGGCTGCACT TTCGTCGCGT TCGGCCCGGC CTCGCGCTT 60
 TTCTTGATCA CTGTGGCTGG GGACCCGCTT CGCGTTATCA TCCTGGTCGC AGGGGCATTT 120
 TTCTGGCTGG TCTCCCTGCT CCTGGCCTCT GTGGTCTGGT TCATCTTGGT CCATGTGACC 180
 GACCGGTCAG ATGCCCGGCT CCAGTACGGC CTCCTGATTT TTGGTGCTGC TGTCTCTGTC 240
 30 CTTCTACAGG AGGTGTTCCG CTTTGCCCTAC TACAAGCTGC TTAAGAAGGC AGATGAGGGG 300
 TTAGCATCGC TGAGTGAGGA CGGAAGATCA CCCATCTCCA TCCGCCAGAT GGCCTATGTT 360
 TCTGGTCTCT CCTTCGGTAT CATCAGTGGT GTCTTCTCTG TTATCAATAT TTTGGCTGAT 420
 GCACTTGGGC CAGGTGTGGT TGGGATCCAT GGAGACTCAC CCTATTACTT CCTGACTTCA 480
 GCCTTTCTGA CAGCAGCCAT TATCCTGCTC CATACTTTT GGGGAGTTGT GTTCTTTGAT 540
 35 GCCTGTGAGA GGAGACGGTA CTGGGCTTTG GGCCTGGTGG TTGGGAGTCA CCTACTGACA 600
 TCGGGACTGA CATTCCTGAA CCCCTGGTAT GAGGCCAGCC TGCTGCCCAT CTATGCAGTC 660
 ACTGTTTCCA TGGGGCTCTG GGCCTTCATC ACAGCTGGAG GGTCCCTCCG AAGTATTCAG 720
 CGCAGCCTCT TGTGTAAGGA C 741

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339

5 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10424

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGAACTTCT	ATTACTCCT	AGCGAGCAGC	ATTCTGTGTG	CCTTGATTGT	CTTCTGAAAA	60
TATCGCCGCT	TTCAGAGAAA	CACTGGCGAA	ATGTCATCAA	ATTCAACTGC	TCTTGCACTA	120
GTGAGACCCT	CTTCTTCTGG	GTTAATTAAC	AGCAATACAG	ACAACAATCT	TGCAGTCTAC	180
20 GACCTCTCTC	GGGATATTTT	AAATAATTTC	CCACACTCAA	TAGCCAGGCA	GAAGCGAATA	240
TTGGTAAACC	TCAGTATGGT	GGAAAACAAG	CTGGTTGAAC	TGGAACATAC	TCTACTTAGC	300
AAGGGTTTCA	GAGGTGCATC	ACCTCACCGG	AAATCCACC			339

25 (2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1095

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

30 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

35 (B) CELL KIND: Epidermoid carcinoma

(C) CELL LINE: KB

(D) CLONE NAME: HP10428

116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

	ATGGGGAGGT GGGCCCTCGA TGTGGCCTTT TTGTGGAAGG CCGTGTTGAC CCTGGGGCTG	60
	GTGCTTCTCT ACTACTGCTT CTCCATCGGC ATCACCTTCT ACAACAAGTG GCTGACAAAG	120
5	AGCTTCCATT TCCCCCTCTT CATGACGATG CTGCACCTGG CCGTGATCTT CCTCTTCTCC	180
	GCCCTGTCCA GGGCGCTGGT TCAGTGCTCC AGCCACAGGG CCCGTGTGGT GCTGAGCTGG	240
	GGCGACTACC TCAGAAGAGT GGCTCCCACA GCTCTGGCGA CGGCGCTTGA CGTGGGCTTG	300
	TCCAACTGGA GCTTCCTGTA TGTCACCGTC TCGCTGTACA CAATGACCAA ATCCTCAGCT	360
	GTCTCTTCA TCTTGATCTT CTCTCTGATC TTCAAGCTGG AGGAGCTGCG CGCGGCACTG	420
10	GTCTGGTGG TCCTCCTCAT CGCCGGGGGT CTCTTCATGT TCACCTACAA GTCCACACAG	480
	TTCAACGTGG AGGGCTTCGC CTTGGTGCTG GGGGCCTCGT TCATCGGTGG CATTGCTGG	540
	ACCTCACCC AGATGCTCCT GCAGAAGGCT GAACTCGGCC TCCAGAATCC CATCGACACC	600
	ATGTTCCACC TGCAGCCACT CATGTTCTTG GGGCTCTTCC CTCTCTTTGC TGTATTTGAA	660
	GGTCTCCATT TGTCCACATC TGAGAAAATC TTCCGTTTCC AGGACACAGG GCTGCTCCTG	720
15	CGGGTACTTG GGAGCCTCTT CCTTGGCGGG ATTCTCGCCT TTGGTTTGGG CTTCTCTGAG	780
	TTCCTCCTGG TCTCCAGAAC CTCCAGCCTC ACTCTCTCCA TTGCCGGCAT TTTTAAGGAA	840
	GTCTGCACTT TGCTGTTGGC AGCTCATCTG CTGGGCGATC AGATCAGCCT CCTGAACTGG	900
	CTGGGCTTCG CCCTCTGCCT CTCGGAATA TCCCTCCACG TTGCCCTCAA AGCCCTGCAT	960
	TCCAGAGGTG ATGGTGGCCC CAAGGCCTTG AAGGGCTGG GCTCCAGCCC CGACCTGGAG	1020
20	CTGCTGCTCC GGAGCAGCCA GCGGGAGGAA GGTGACAATG AGGAGGAGGA GTACTTTGTG	1080
	GCCCAGGGGC AGCAG	1095

(2) INFORMATION FOR SEQ ID NO: 33:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 678
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 30 (ii) SEQUENCE KIND: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
 - (B) CELL KIND: Stomach cancer
 - (D) CLONE NAME: HP10429
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

117

ATGCCTACCA CAAAGAAGAC ATTGATGTTT TTATCAAGCT TTTTCACCAG CCTTGGGTCC 60
 TTCATTGTAA TTTGCTCTAT TCTTGGGACA CAAGCATGGA TCACCAGTAC AATTGCTGTT 120
 AGAGACTCTG CTTCAAATGG GAGCATT TTC ATCACTTACG GACTTTTTTCG TGGGGAGAGT 180
 AGTGAAGAAT TGAGTCACGG ACTTGCAGAA CCAAAGAAAA AGTTTGCAGT TTTAGAGATA 240
 5 CTGAATAATT CTTCCCAAAA AACTCTGCAT TCGGTGACTA TCCTGTTTCT GGTCTGAGT 300
 TTGATCACGT CGCTGCTGAG CTCTGGGTTT ACCTTCTACA ACAGCATCAG CAACCCTTAC 360
 CAGACATTCC TGGGGCCGAC GGGGGTGAC ACCTGGAACG GGCTCGGTGC ATCCTTCGTT 420
 TTTGTGACCA TGATACTGTT TGTGGCGAAC ACGCAGTCCA ACCAACTCTC CGAAGAGTTG 480
 TTCCAAATGC TTTACCCGGC AACCACCAGT AAAGGAACGA CCCACAGTTA CGGATACTCG 540
 10 TTCTGGCTCA TACTGCTCGT CATCTTCTA AATATAGTCA CTGTAACCAT CATCATTTTC 600
 TACCAGAAGG CCAGATACCA GCGGAAGCAG GAGCAGAGAA AGCCAATGGA ATATGCTCCA 660
 AGGGACGGAA TTTTATTC 678

15 (2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP10432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

30 ATGGCTCGGG GCTCGCTGCG CCGGTTGCTG CGGCTCCTCG TGCTGGGGCT CTGGCTGGCG 60
 TTGCTGCGCT CCGTGCCCGG GGAGCAAGCG CCAGGCACCG CCCCTGCTC CCGCGGCAGC 120
 TCCTGGAGCG CGGACCTGGA CAAGTGCATG GACTGCGCGT CTTGCAGGGC GCGACCGCAC 180
 AGCGACTTCT GCCTGGGCTG CGCTGCAGCA CCTCTGCC CTTCCGGCT GCTTTGGCCC 240
 35 ATCCTTGGGG GCGCTCTGAG CCTGACCTTC GTGCTGGGGC TGCTTTCTGG CTTTTGGTTC 300
 TGGAGACGAT GCCGCAGGAG AGAGAAGTTC ACCACCCCA TAGAGGAGAC CGGCGGAGAG 360
 GGCTGCCCAG CTGTGGCGCT GATCCAG 387

118

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489

(B) TYPE: Nucleic acid

5 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP10433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

15

```
ATGCGACGGC TGCTGATCCC TCTGGCCCTG TGGCTGGGCG CGGTGGGCGT GGGCGTCGCC      60
GAGCTCACGG AAGCCCAGCG CCGGGGCTTG CAGGTGGCCC TGGAGGAATT TCACAAGCAC      120
CCGCCCCGTG AGTGGGCCTT CCAGGAGACC AGTGTGGAGA GCGCCGTGGA CACGCCCTTC      180
CCAGCTGGAA TATTGTGAG GCTGGAATTT AAGCTGCAGC AGACAAGCTG CCGGAAGAGG      240
20 GACTGGAAGA AACCCGAGTG CAAAGTCAGG CCAATGGGA GGAAACGGAA ATGCCTGGCC      300
TGCATCAAAC TGGGCTCTGA GGACAAAGTT CTGGGCCGGT TGGTCCACTG CCCCATAGAG      360
ACCCAAGTTC TCGGGGAGGC TGAGGAGCAC CAGGAGACCC AGTGCCTCAG GGTGCAGCGG      420
GCTGGTGAGG ACCCCACAG CTTCTACTTC CCTGGACAGT TCGCCTTCTC CAAGGCCCTG      480
CCCCGCAGC                                     489
```

25

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

	ATGATCCGCT	GCGGCCTGGC	CTGCGAGCGC	TGCCGCTGGA	TCCTGCCOCT	GCTCCTACTC	60
	AGCGCCATCG	CCTTCGACAT	CATCGCGCTG	GCCGGCCGCG	GCTGGTTGCA	GTCTAGCGAC	120
5	CACGGCCAGA	CGTCCCTCGCT	GTGGTGGA	TGCTCCCAAG	AGGGCGGCGG	CAGCGGGTCC	180
	TACGAGGAGG	GCTGTCAGAG	CCTCATGGAG	TACGCGTGGG	GTAGAGCAGC	GGCTGCCATG	240
	CTCTTCTGTG	GCTTCATCAT	CCTGGTGATC	TGTTTCATCC	TCTCCTTCTT	CGCCCTCTGT	300
	GGACCCCA	TGCTTGCTTT	CCTGAGAGTG	ATTGGAGGTC	TCCTTGCCCTT	GGCTGCTGTG	360
	TTCCAGATCA	TCTCCCTGGT	AATTTACCCC	GTGAAGTACA	CCCAGACCTT	CACCCTTCAT	420
10	GCCAACCGTG	CTGTCACTTA	CATCTATAAC	TGGGCCTACG	GCTTTGGGTG	GGCAGCCACG	480
	ATTATCCTGA	TCGGCTGTGC	CTTCTTCTTC	TGCTGCCTCC	CCAACTACGA	AGATGACCTT	540
	CTGGGCAATG	CCAAGCCCAG	GTACTTCTAC	ACATCTGCC			579

15 (2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1502

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP01263

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

30 (B) EXISTENCE POSITION: 37.. 1185

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

35 ACAAACGAC CCATCCTGGG CCTTGTTCTC CACAGA ATG GGT CTG CTC CTT CCC 54
 Met Gly Leu Leu Leu Pro
 1 5

CTG GCA CTC TGC ATC CTA GTC CTG TGC TGC GGA GCA ATG TCT CCA CCC 102

120

	Leu Ala Leu Cys Ile Leu Val L u Cys Cys Gly Ala M t S r Pro Pro	
	10 15 20	
	CAG CTG GCC CTC AAC CCC TCG GCT CTG CTC TCC CGG GGC TGC AAT GAC	150
	Gln Leu Ala Leu Asn Pro Ser Ala Leu Leu Ser Arg Gly Cys Asn Asp	
5	25 30 35	
	TCC GAT GTG CTG GCA GTT GCA GGC TTT GCC CTG CGG GAT ATT AAC AAA	198
	Ser Asp Val Leu Ala Val Ala Gly Phe Ala Leu Arg Asp Ile Asn Lys	
	40 45 50	
	GAC AGA AAG GAT GGC TAT GTG CTG AGA CTC AAC CGA GTG AAC GAC GCC	246
10	Asp Arg Lys Asp Gly Tyr Val Leu Arg Leu Asn Arg Val Asn Asp Ala	
	55 60 65 70	
	CAG GAA TAC AGA CGG GGT GGC CTG GGA TCT CTG TTC TAT CTT ACA CTG	294
	Gln Glu Tyr Arg Arg Gly Gly Leu Gly Ser Leu Phe Tyr Leu Thr Leu	
	75 80 85	
15	GAT GTG CTA GAG ACT GAC TGC CAT GTG CTC AGA AAG AAG GCA TGG CAA	342
	Asp Val Leu Glu Thr Asp Cys His Val Leu Arg Lys Lys Ala Trp Gln	
	90 95 100	
	GAC TGT GGA ATG AGG ATA TTT TTT GAA TCA GTT TAT GGT CAA TGC AAA	390
	Asp Cys Gly Met Arg Ile Phe Phe Glu Ser Val Tyr Gly Gln Cys Lys	
20	105 110 115	
	GCA ATA TTT TAT ATG AAC AAC CCA AGT AGA GTT CTC TAT TTA GCT GCT	438
	Ala Ile Phe Tyr Met Asn Asn Pro Ser Arg Val Leu Tyr Leu Ala Ala	
	120 125 130	
	TAT AAC TGT ACT CTT CGC CCA GTT TCA AAA AAA AAG ATT TAC ATG ACG	486
25	Tyr Asn Cys Thr Leu Arg Pro Val Ser Lys Lys Lys Ile Tyr Met Thr	
	135 140 145 150	
	TGC CCT GAC TGC CCA AGC TCC ATA CCC ACT GAC TCT TCC AAT CAC CAA	534
	Cys Pro Asp Cys Pro Ser Ser Ile Pro Thr Asp Ser Ser Asn His Gln	
	155 160 165	
30	GTG CTG GAG GCT GCC ACC GAG TCT CTT GCG AAA TAC AAC AAT GAG AAC	582
	Val Leu Glu Ala Ala Thr Glu Ser Leu Ala Lys Tyr Asn Asn Glu Asn	
	170 175 180	
	ACA TCC AAG CAG TAT TCT CTC TTC AAA GTC ACC AGG GCT TCT AGC CAG	630
	Thr Ser Lys Gln Tyr Ser Leu Phe Lys Val Thr Arg Ala Ser Ser Gln	
35	185 190 195	
	TGG GTG GTC GGC CCT TCT TAC TTT GTG GAA TAC TTA ATT AAA GAA TCA	678
	Trp Val Val Gly Pro Ser Tyr Phe Val Glu Tyr Leu Ile Lys Glu Ser	
	200 205 210	

121

	CCA TGT ACT AAA TCC CAG GCC AGC AGC TGT TCA CTT CAG TCC TCC GAC	726
	Pro Cys Thr Lys Ser Gln Ala Ser Ser Cys Ser Leu Gln Ser Ser Asp	
	215 220 225 230	
	TCT GTG CCT GTT GGT CTT TGC AAA GGT TCT CTG ACT CGA ACA CAC TGG	774
5	Ser Val Pro Val Gly Leu Cys Lys Gly Ser Leu Thr Arg Thr His Trp	
	235 240 245	
	GAA AAG TTT GTC TCT GTG ACT TGT GAC TTC TTT GAA TCA CAG GCT CCA	822
	Glu Lys Phe Val Ser Val Thr Cys Asp Phe Phe Glu Ser Gln Ala Pro	
	250 255 260	
10	GCC ACT GGA AGT GAA AAC TCT GCT GTT AAC CAG AAA CCT ACA AAC CTT	870
	Ala Thr Gly Ser Glu Asn Ser Ala Val Asn Gln Lys Pro Thr Asn Leu	
	265 270 275	
	CCC AAG GTG GAA GAA TCC CAG CAG AAA AAC ACC CCC CCA ACA GAC TCC	918
	Pro Lys Val Glu Glu Ser Gln Gln Lys Asn Thr Pro Pro Thr Asp Ser	
15	280 285 290	
	CCC TCC AAA GCT GGG CCA AGA GGA TCT GTC CAA TAT CTT CCT GAC TTG	966
	Pro Ser Lys Ala Gly Pro Arg Gly Ser Val Gln Tyr Leu Pro Asp Leu	
	295 300 305 310	
	GAT GAT AAA AAT TCC CAG GAA AAG GGC CCT CAG GAG GCC TTT CCT GTG	1014
20	Asp Asp Lys Asn Ser Gln Glu Lys Gly Pro Gln Glu Ala Phe Pro Val	
	315 320 325	
	CAT CTG GAC CTA ACC ACG AAT CCC CAG GGA GAA ACC CTG GAT ATT TCC	1062
	His Leu Asp Leu Thr Thr Asn Pro Gln Gly Glu Thr Leu Asp Ile Ser	
	330 335 340	
25	TTC CTC TTC CTG GAG CCT ATG GAG GAG AAG CTG GTT GTC CTG CCT TTC	1110
	Phe Leu Phe Leu Glu Pro Met Glu Glu Lys Leu Val Val Leu Pro Phe	
	345 350 355	
	CCC AAA GAA AAA GCA CGC ACT GCT GAG TGC CCA GGG CCA GCC CAG AAT	1158
	Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys Pro Gly Pro Ala Gln Asn	
30	360 365 370	
	GCC AGC CCT CTT GTC CTT CCG CCA TGAGAATCAC ACAGAGTCTT CTGTAGGG	1210
	Ala Ser Pro Leu Val Leu Pro Pro	
	375 380	
	GTATGGTGCG CCGCATGACA TGGGAGGCCA TGGGGACGAT GGACAGAGAC AGAGCGTGCA	1270
35	CACGTAGAGT GGCTAGTGAA GGACGCCTTT TTGACTCTTC TTGGTCTCAG CATGTTGACT	1330
	GGGATTGGAA ATAATGAGAC TGAGCCCTCG GCTTGGGCTG CACTCTACCC TGTACACTGC	1390
	CTTGTACCCT GAGCTGCATC ACCTCCTAAA CTGAGCAGTC TCATACCATG GAGAGATGCC	1450
	TCTCTTATGT CTTAGCCAC TCACTTATAA AGATACTTAT CTTTTCAGCA GT	1502

122

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1349

5 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP01299

15

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 111.. 1064

(C) CHARACTERIZATION METHOD: E

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

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AGCAGTTGGG GCAGGAGGAA GCCGACTGCT GCCTGGTCTG CAAAGAAGTC CTTTCAAGTC      60
TCTAGGACTG GACTCTTCCT AAGCAAGTCC GAGAAGGAAG CACCCTCACT ATG TGG      116
25                                     Met Trp
                                     1
CTC TAC CTG GCG GCC TTC GTG GGC CTG TAC TAC CTT CTG CAC TGG TAC
164
Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His Trp Tyr
30          5              10              15
CGG GAG AGG CAG GTG GTG AGC CAC CTC CAA GAC AAG TAT GTC TTT ATC      212
Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val Phe Ile
          20              25              30
ACG GGC TGT GAC TCG GGC TTT GGG AAC CTG CTG GCC AGA CAG CTG GAT      260
35 Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln Leu Asp
          35              40              45              50
GCA CGA GGC TTG AGA GTG CTG GCT GCG TGT CTG ACG GAG AAG GGG GCC      308
Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys Gly Ala

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123

		55		60		65		
		GAG CAG CTG AGG GGC CAG ACG TCT GAC AGG CTG GAG ACG GTG ACC CTG						356
		Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val Thr Leu						
		70		75		80		
5		GAT GTT ACC AAG ATG GAG AGC ATC GCT GCA GCT ACT CAG TGG GTG AAG						404
		Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp Val Lys						
		85		90		95		
		GAG CAT GTG GGG GAC AGA GGA CTC TGG GGA CTG GTG AAC AAT GCA GGC						452
		Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn Ala Gly						
10		100		105		110		
		ATT CTT ACA CCA ATT ACC TTA TGT GAG TGG CTG AAC ACT GAG GAC TCT						500
		Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu Asp Ser						
		115		120		125		130
		ATG AAT ATG CTC AAA GTG AAC CTC ATT GGT GTG ATC CAG GTG ACC TTG						548
15		Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val Thr Leu						
		135		140		145		
		AGC ATG CTT CCT TTG GTG AGG AGA GCA CGG GGA AGA ATT GTC AAT GTC						596
		Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val Asn Val						
		150		155		160		
20		TCC AGC ATT CTG GGA AGA GTT GCT TTC TTT GTA GGA GGC TAC TGT GTC						644
		Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr Cys Val						
		165		170		175		
		TCC AAG TAT GGA GTG GAA GCC TTT TCA GAT ATT CTG AGG CGT GAG ATT						692
		Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg Glu Ile						
25		180		185		190		
		CAA CAT TTT GGG GTG AAA ATC AGC ATA GTT GAA CCT GGC TAC TTC AGA						740
		Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr Phe Arg						
		195		200		205		210
		ACG GGA ATG ACA AAC ATG ACA CAG TCC TTA GAG CGA ATG AAG CAA AGT						788
30		Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys Gln Ser						
		215		220		225		
		TGG AAA GAA GCC CCC AAG CAT ATT AAG GAG ACC TAT GGA CAG CAG TAT						836
		Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln Gln Tyr						
		230		235		240		
35		TTT GAT GCC CTT TAC AAT ATC ATG AAG GAA GGG CTG TTG AAT TGT AGC						884
		Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu Leu Asn Cys Ser						
		245		250		255		
		ACA AAC CTG AAC CTG GTC ACT GAC TGC ATG GAA CAT GCT CTG ACA TCG						932

124

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Thr Asn Leu Asn Leu Val Thr Asp Cys Met Glu His Ala Leu Thr Ser
    260                      265                      270
GTG CAT CCG CGA ACT CGA TAT TCA GCT GGC TGG GAT GCT AAA TTT TTC      980
Val His Pro Arg Thr Arg Tyr Ser Ala Gly Trp Asp Ala Lys Phe Phe
5  275                      280                      285                      290
TTC ATC CCT CTA TCT TAT TTA CCT ACA TCA CTG GCA GAC TAC ATT TTG      1028
Phe Ile Pro Leu Ser Tyr Leu Pro Thr Ser Leu Ala Asp Tyr Ile Leu
                      295                      300                      305
ACT AGA TCT TGG CCC AAA CCA GCC CAG GCA GTC TAAAGAAAAC TGGGTTGGT      1080
10 Thr Arg Ser Trp Pro Lys Pro Ala Gln Ala Val
    310                      315
GCTTCTTGGA ATGAAGGCAA AAATCTGAAA TTGTTAGTGT CTCAGTAATC CTGATTTAGA      1140
ACCCAGGCTT TTTGTAACAA TGTGTTTTCT TGCCTAAATT CATTTATCTG GCATCATCAG      1200
AGTACTAACA TGTTTATATT TCAGATATCC AAAGCTTACC ACTTTAGGTG ATGAATCTTT      1260
15 ACTATTTTAG CCCTTTTTTG ATGAGACTAT TTGTCTAAAG TGAATCATTT GTTCTTGCCCT      1320
TATTAAACAG AGTAGATGGA AAACAATTT      1349

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(2) INFORMATION FOR SEQ ID NO: 39:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1643
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 25 (ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
 - (B) CELL KIND: Liver
 - (D) CLONE NAME: HP01347
- 30

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
 - (B) EXISTENCE POSITION: 25.. 915
 - (C) CHARACTERIZATION METHOD: E
- 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

125

	AACATCTGGG GACAGCGGGA AAAC ATG AGT GAC TCC AAG GAA CCA AGG GTG	51
	Met Ser Asp Ser Lys Glu Pro Arg Val	
	1 5	
	CAG CAG CTG GGC CTC CTG GGG TGT CTT GGC CAT GGC GCC CTG GTG CTG	99
5	Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu	
	10 15 20 25	
	CAA CTC CTC TCC TTC ATG CTC TTG GCT GGG GTC CTG GTG GCC ATC CTT	147
	Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu	
	30 35 40	
10	GTC CAA GTG TCC AAG GTC CCC AGC TCC CTA AGT CAG GAA CAA TCC GAG	195
	Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu	
	45 50 55	
	CAA GAC GCA ATC TAC CAG AAC CTG ACC CAG CTT AAA GCT GCA GTG GGT	243
	Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly	
15	60 65 70	
	GAG CTC TCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACC	291
	Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr	
	75 80 85	
	CAG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG	339
20	Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln	
	90 95 100 105	
	GAG ATC TAC CAG GAG CTG ACC CGG CTG AAG GCT GCA GTG GGT GAG TTG	387
	Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala-Ala Val Gly Glu Leu	
	110 115 120	
25	CCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACC CGG CTG	435
	Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu	
	125 130 135	
	AAG GCT GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG GAG ATC	483
	Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile	
30	140 145 150	
	TAC CAG GAG CTG ACC CGG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAG	531
	Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu	
	155 160 165	
	AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACG GAG CTG AAG GCT	579
35	Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala	
	170 175 180 185	
	GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG	627
	Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln	

126

	190	195	200	
	GAG CTG ACC CAG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAC CAG TCC			675
	Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser			
	205	210	215	
5	AAG CAG CAG CAA ATC TAT CAA GAA CTG ACC GAT TTG AAG ACT GCA TTT			723
	Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe			
	220	225	230	
	GAA CGC CTG TGC CGC CAC TGT CCC AAG GAC TGG ACA TTC TTC CAA GGA			771
	Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly			
10	235	240	245	
	AAC TGT TAC TTC ATG TCT AAC TCC CAG CGG AAC TGG CAC GAC TCC GTC			819
	Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val			
	250	255	260	265
	ACC GCC TGC CAG GAA GTG AGG GCC CAG CTC GTC GTA ATC AAA ACT GCT			867
15	Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala			
	270	275	280	
	GAG GAG CAG CTT CCA GCG GTA CTG GAA CAG TGG AGA ACC CAA CAA			912
	Glu Glu Gln Leu Pro Ala Val Leu Glu Gln Trp Arg Thr Gln Gln			
	285	290	295	
20	TAGCGGGAAT GAAGACTGTG CGGAATTTAG TGGCAGTGGC TGGAACGACA ATCGATGT			970
	GACGTTGACA ATTACTGGAT CTGCAAAAAG CCCGCAGCCT GCTTCAGAGA CGAATAGTTG			1030
	TTTCCCTGCT AGCCTCAGCC TCCATTGTGG TATAGCAGAA CTTCACCCAC TTGTAAGCCA			1090
	GCGCTTCTTC TCTCCATCCT TGGACCTTCA CAAATGCCCT GAGACGGTTC TCTGTTCGAT			1150
	TTTTCATCCC CTATGAACCT GGGTCTTATT CTGTCCTTCT GATGCCTCCA AGTTTCCCTG			1210
25	GTGTAGAGCT TGTGTTCTTG GCCCATCCTT GGAGCTTTAT AAGTGACCTG AGTGGGATGC			1270
	ATTTAGGGGG CGGGCTTGGT ATGTTGTATG AATCCACTCT CTGTTCCTTT TGGAGATTAG			1330
	ACTATTTGGA TTCATGTGTA GCTGCCCTGT CCCCTGGGGC TTTATCTCAT CCATGCAAAC			1390
	TACCATCTGC TCAACTTCCA GCTACACCCC GTGCACCCTT TTGACTGGGG ACTTGCTGGT			1450
	TGAAGGAGCT CATCTTGCAG GCTGGAAGCA CCAGGGAATT AATTCCCCCA GTCAACCAAT			1510
30	GGCATCCAGA GAGGGCATGG AGGCTCCATA CAACCTCTTC CACCCCACA TCTTTCTTTG			1570
	TCCTATACAT GTCTTCATT TGGCTGTTTC TGAGTTGTAG CCTTTATAAT AAAGTGGTAA			1630
	ATGTTGTAAC TGC			1643

35 (2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729

(B) TYPE: Nucleic acid

127

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01440

10 (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 38.. 631

(C) CHARACTERIZATION METHOD: E

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

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ACTTTCACTC ACCGCCTGTC CTCCTGACA CCTCACC ATG TGT ACG GGA AAA TGT      55
                                     Met Cys Thr Gly Lys Cys
                                     1           5
20 GCC CGC TGT GTG GGG CTC TCC CTC ATT ACC CTC TGC CTC GTC TGC ATT      103
   Ala Arg Cys Val Gly Leu Ser Leu Ile Thr Leu Cys Leu Val Cys Ile
       10           15           20
   GTG GCC AAC GCC CTC CTG CTG GTA CCT AAT GGG GAG ACC TCC TGG ACC      151
   Val Ala Asn Ala Leu Leu Leu Val Pro Asn Gly Glu Thr Ser Trp Thr
25       25           30           35
   AAC ACC AAC CAT CTC AGC TTG CAA GTC TGG CTC ATG GGC GGC TTC ATT      199
   Asn Thr Asn His Leu Ser Leu Gln Val Trp Leu Met Gly Gly Phe Ile
       40           45           50
   GGC GGG GGC CTA ATG GTA CTG TGT CCG GGG ATT GCA GCC GTT CGG GCA      247
30 Gly Gly Gly Leu Met Val Leu Cys Pro Gly Ile Ala Ala Val Arg Ala
   55           60           65           70
   GGG GGC AAG GGC TGC TGT GGT GCT GGG TGC TGT GGA AAC CGC TGC AGG      295
   Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys Cys Gly Asn Arg Cys Arg
       75           80           85
35 ATG CTG CGC TCG GTC TTC TCC TCG GCG TTC GGG GTG CTT GGT GCC ATC      343
   Met Leu Arg Ser Val Phe Ser Ser Ala Phe Gly Val Leu Gly Ala Ile
       90           95           100
   TAC TGC CTC TCG GTG TCT GGA GCT GGG CTC CGA AAT GGA CCC AGA TGC      391

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128

Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu Arg Asn Gly Pro Arg Cys
 105 110 115
 TTA ATG AAC GGC GAG TGG GGC TAC CAC TTC GAA GAC ACC GCG GGA GCT 439
 Leu Met Asn Gly Glu Trp Gly Tyr His Phe Glu Asp Thr Ala Gly Ala
 5 120 125 130
 TAC TTG CTC AAC CGC ACT CTA TGG GAT CGG TGC GAG GCG CCC CCT CGC 487
 Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg Cys Glu Ala Pro Pro Arg
 135 140 145 150
 GTG GTC CCC TGG AAT GTG ACG CTC TTC TCG CTG CTG GTG GCC GCC TCC 535
 10 Val Val Pro Trp Asn Val Thr Leu Phe Ser Leu Leu Val Ala Ala Ser
 155 160 165
 TGC CTG GAG ATA GTA CTG TGT GGG ATC CAG CTG GTG AAC GCG ACC ATT 583
 Cys Leu Glu Ile Val Leu Cys Gly Ile Gln Leu Val Asn Ala Thr Ile
 170 175 180
 15 GGT GTC TTC TGC GGC GAT TGC AGG AAA AAA CAG GAC ACC CCT CAC TG 630
 Gly Val Phe Cys Gly Asp Cys Arg Lys Lys Gln Asp Thr Pro His
 185 190 195
 AGGCTCCACT GACCGCCGGG TTACACCTGC TCCTTCCTGG ACGCCTACCT GGCTCGCTCA 690
 CTCCTTGCT CGCTAGAATA AACTGCTTTG CGCTCTCTT 729
 20

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1322

25 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01526

35 (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 84.. 749

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

	GAGCCGCAGG TCTGGGCTGC AGTAGGTCCC GGCAACCGCA GGCTCGCGGC GGGCGCTGGG	60
	CGCGGGATCC GACTCTAGTC GTA ATG GAG GCG GGC GGC TTT CTG GAC TCG CTC	113
5	Met Glu Ala Gly Gly Phe Leu Asp Ser Leu	
	1 5 10	
	ATT TAC GGA GCA TGC GTG GTC TTC ACC CTT GGC ATG TTC TCC GCC GGC	161
	Ile Tyr Gly Ala Cys Val Val Phe Thr Leu Gly Met Phe Ser Ala Gly	
	15 20 25	
10	CTC TCG GAC CTC AGG CAC ATG CGA ATG ACC CGG AGT GTG GAC AAC GTC	209
	Leu Ser Asp Leu Arg His Met Arg Met Thr Arg Ser Val Asp Asn Val	
	30 35 40	
	CAG TTC CTG CCC TTT CTC ACC ACG GAA GTC AAC AAC CTG GGC TGG CTG	257
	Gln Phe Leu Pro Phe Leu Thr Thr Glu Val Asn Asn Leu Gly Trp Leu	
15	45 50 55	
	AGT TAT GGG GCT TTG AAG GGA GAC GGG ATC CTC ATC GTC GTC AAC ACA	305
	Ser Tyr Gly Ala Leu Lys Gly Asp Gly Ile Leu Ile Val Val Asn Thr	
	60 65 70	
	GTG GGT GCT GCG CTT CAG ACC CTG TAT ATC TTG GCA TAT CTG CAT TAC	353
20	Val Gly Ala Ala Leu Gln Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr	
	75 80 85 90	
	TGC CCT CGG AAG CGT GTT GTG CTC CTA CAG ACT GCA ACC CTG CTA GGG	401
	Cys Pro Arg Lys Arg Val Val Leu Leu Gln Thr Ala Thr Leu Leu Gly	
	95 100 105	
25	GTC CTT CTC CTG GGT TAT GGC TAC TTT TGG CTC CTG GTA CCC AAC CCT	449
	Val Leu Leu Leu Gly Tyr Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro	
	110 115 120	
	GAG GCC CGG CTT CAG CAG TTG GGC CTC TTC TGC AGT GTC TTC ACC ATC	497
	Glu Ala Arg Leu Gln Gln Leu Gly Leu Phe Cys Ser Val Phe Thr Ile	
30	125 130 135	
	AGC ATG TAC CTC TCA CCA CTG GCT GAC TTG GCT AAG GTG ATT CAA ACT	545
	Ser Met Tyr Leu Ser Pro Leu Ala Asp Leu Ala Lys Val Ile Gln Thr	
	140 145 150	
	AAA TCA ACC CAA TGT CTC TCC TAC CCA CTC ACC ATT GCT ACC CTT CTC	593
35	Lys Ser Thr Gln Cys Leu Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu	
	155 160 165 170	
	ACC TCT GCC TCC TGG TGC CTC TAT GGG TTT CGA CTC AGA GAT CCC TAT	641
	Thr Ser Ala Ser Trp Cys Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr	

130

	175	180	185	
	ATC ATG GTG TCC AAC TTT CCA GGA ATC GTC ACC AGC TTT ATC CGC TTC			689
	Ile Met Val Ser Asn Phe Pro Gly Ile Val Thr Ser Phe Ile Arg Phe			
	190	195	200	
5	TGG CTT TTC TGG AAG TAC CCC CAG GAG CAA GAC AGG AAC TAC TGG CTC			737
	Trp Leu Phe Trp Lys Tyr Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu			
	205	210	215	
	CTG CAA ACC TGAGGCTGCT CATCTGACCA CTGGGCACCT TAGTGCCAAC CTGA			790
	Leu Gln Thr			
10	220			
	ACCAAAGAGA CCTCCTTGTT TCAGCTGGGC CTGCTGTCCA GCTTCCCAGG TGCAGTGGGT			850
	TGTGGGAACA AGAGATGACT TTGAGGATAA AAGGACCAAA GAAAAAGCTT TACTTAGATG			910
	ATTGATTGGG GCCTAGGAGA TGAAATCACT TTTTATTTTT TAGAGATTTT TTTTTTTAAT			970
	TTTGGAGGTT GGGGTGCAAT CTTTGAATA TGCCTTAAAA GGCCGGGCGC GGTGGCTCAC			1030
15	GCCTGTAATC CCAGCACTTT GGGAGGCCAA GGTGGGCGGA TCGCCTGAGG TCAGGAGTTC			1090
	AAGACCAACC TGAATAACAT GGTGAAACCC CATCTCTACT AAAAATACAA AATTAGCCAG			1150
	GCGATGATGC ACATGCCTGT AATCCCAGAT ACTTGGGAGG CTGAGGCAGG AGAATTGCTT			1210
	GAACCCAGGA GGTGGAGGTT GCAGTGAGCT GAGATCGTGC CATTGTGATA TGAATATGCC			1270
	TTATATGCTG ATATGAATAT GCCTTAAAAA AAAGTGTTCC CCACCCCTGC CC			1322
20				

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3045
- 25 (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) SEQUENCE KIND: cDNA to mRNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10230

35 (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 191.. 946
- (C) CHARACTERIZATION METHOD: E

131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

	GTTCGCCTC AGAAGGCTGC CTCGCTGGTC CGAATTCGGT GCGCCACGT CCGCCGTCT	60
	CCGCCTTCTG CATCGCGGCT TCGGCGGCTT CCACCTAGAC ACCTAACAGT CGCGGAGCCG	120
5	GCCGCGTCGT GAGGGGGTCG GCACGGGGAG TCGGCGGTC TTGTGCATCT TGGCTACCTG	180
	TGGGTCGAAG ATG TCG GAC ATC GGA GAC TGG TTC AGG AGC ATC CCG GCG	229
	Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala	
	1 5 10	
	ATC ACG CGC TAT TGG TTC GCC GCC ACC GTC GCC GTG CCC TTG GTC GGC	277
10	Ile Thr Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly	
	15 20 25	
	AAA CTC GGC CTC ATC AGC CCG GCC TAC CTC TTC CTC TGG CCC GAA GCC	325
	Lys Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala	
	30 35 40 45	
15	TTC CTT TAT CGC TTT CAG ATT TGG AGG CCA ATC ACT GCC ACC TTT TAT	373
	Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr	
	50 55 60	
	TTC CCT GTG GGT CCA GGA ACT GGA TTT CTT TAT TTG GTC AAT TTA TAT	421
	Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr	
20	65 70 75	
	TTC TTA TAT CAG TAT TCT ACG CGA CTT GAA ACA GGA GCT TTT GAT GGG	469
	Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly	
	80 85 90	
	AGG CCA GCA GAC TAT TTA TTC ATG CTC CTC TTT AAC TGG ATT TGC ATC	517
25	Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile	
	95 100 105	
	GTG ATT ACT GGC TTA GCA ATG GAT ATG CAG TTG CTG ATG ATT CCT CTG	565
	Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu	
	110 115 120 125	
30	ATC ATG TCA GTA CTT TAT GTC TGG GCC CAG CTG AAC AGA GAC ATG ATT	613
	Ile Met Ser Val Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile	
	130 135 140	
	GTA TCA TTT TGG TTT GGA ACA CGA TTT AAG GCC TGC TAT TTA CCC TGG	661
	Val Ser Phe Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp	
35	145 150 155	
	GTT ATC CTT GGA TTC AAC TAT ATC ATC GGA GGC TCG GTA ATC AAT GAG	709
	Val Ile Leu Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu	
	160 165 170	

132

	CTT ATT GGA AAT CTG GTT GGA CAT CTT TAT TTT TTC CTA ATG TTC AGA	757
	Leu Ile Gly Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg	
	175 180 185	
	TAC CCA ATG GAC TTG GGA GGA AGA AAT TTT CTA TCC ACA CCT CAG TTT	805
5	Tyr Pro Met Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe	
	190 195 200 205	
	TTG TAC CGC TGG CTG CCC AGT AGG AGA GGA GGA GTA TCA GGA TTT GGT	853
	Leu Tyr Arg Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly	
	210 215 220	
10	GTG CCC CCT GCT AGC ATG AGG CGA GCT GCT GAT CAG AAT GGC GGA GGC	901
	Val Pro Pro Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly	
	225 230 235	
	GGG AGA CAC AAC TGG GGC CAG GGC TTT CGA CTT GGA GAC CAG TGAAGGG	950
	Gly Arg His Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln	
15	240 245 250	
	CGGGCCTCGG GCAGCCGCTC CTCTCAAGCC ACATTTCCCTC CCAGTGCTGG GTGCGCTTAA	1010
	CAACTGCGTT CTGGCTAACA CTGTTGGACC TGACCCACAC TGAATGTAGT CTTTCAGTAC	1070
	GAGACAAAGT TTCTTAAATC CCGAAGAAAA ATATAAGTGT TCCACAAGTT TCACGATTCT	1130
	CATTCAAGTC CTTACTGCTG TGAAGAACAA ATACCAACTG TGCAAATTGC AAAACTGACT	1190
20	ACATTTTTTTG GTGTCTTCTC TTCTCCCTT TCCGTCTGAA TAATGGGTTT TAGCGGGTCC	1250
	TAGTCTGCTG GCATTGAGCT GGGGCTGGGT CACCAAACCC TTCCCAAAG GACCCTTATC	1310
	TCTTTCTTGC ACACATGCCT CTCTCCCACT TTTCCCAACC CCCACATTG CAACTAGAAG	1370
	AGGTTGCCCA TAAATTGCT CTGCCCTGA CAGGTTCTGT TATTTATTGA CTTTGGCCAA	1430
	GGCTTGGTCA CAACAATCAT ATTACGTAA TTTTCCCCCT TTGGTGGCAG AACTGTAGCA	1490
25	ATAGGGGGAG AAGACAAGCA GCGGATGAAG CGTTTTCTCA GCTTTTGGAA TTGCTTCGAC	1550
	CTGACATCCG TTGTAACCGT TTGCCACTTC TTCAGATATT TTTATAAAAA AGTACCACTG	1610
	AGTCAGTGAG GGCCACAGAT TGGTATTAAT GAGATACGAG GGTGTTGCT GGGTGTGTTGT	1670
	TTCTGAGCT AAGTGATCAA GACTGTAGTG GAGTTGCAGC TAACATGGGT TAGGTTTAAA	1730
	CCGTGGGGGA TGCAACCCCT TTGCGTTTCA TATGTAGGCC TACTGGCTTT GTGTAGCTGG	1790
30	AGTAGTTGGG TTGCTTTGTG TTAGGAGGAT CCAGATCATG TTGGCTACAG GGAGATGCTC	1850
	TCTTTGAGAG GCTCCTGGGC ATTGATTCCA TTTCAATCTC ATTCTGGATA TGTGTTTATT	1910
	GAGTAAAGGA GGAGAGACCC TCATACGCTA TTTAAATGTC ACTTTTTTGC CTATCCCCCG	1970
	TTTTTTGGTC ATGTTTCAAT TAATTGTGAG GAAGGCGCAG CTCCTCTCTG CACGTAGATC	2030
	ATTTTTTAAA GCTAATGTAA GCACATCTAA GGAATAACA TGATTTAAGG TTGAAATGGC	2090
35	TTTAGAATCA TTTGGGTTTG AGGGTGTGTT ATTTTGAGTC ATGAATGTAC AAGCTCTGTG	2150
	AATCAGACCA GCTTAAATAC CCACACCTTT TTTTCGTAGG TGGGCTTTTC CTATCAGAGC	2210
	TTGGCTCATA ACCAAATAAA GTTTTTTGAA GGCCATGGCT TTTACACAG TTATTTTATT	2270
	TTATGACGTT ATCTGAAAGC AGACTGTTAG GAGCAGTATT GAGTGGCTGT CACACTTTGA	2330

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GGCAACTAAA AAGGCTTCAA ACGTTTTGAT CAGTTTCTTT TCAGGAAACA TTGTGCTCTA 2390
ACAGTATGAC TATTCTTTCC CCCACTCTTA AACAGTGTGA TGTGTGTTAT CCTAGGAAAT 2450
GAGAGTTGGC AAACAACCTC TCATTTTGAA TAGAGTTTGT GTGTACCTCT CCATATTTAA 2510
TTTATATGAT AAAATAGGTG GGGAGAGTCT GAACCTTAAC TGTCATGTTT TGTGTTCAT 2570
5 CTGTGGCCAC AATAAGTTT ACTTGTAATA TTTTAGAGGC CATTACTCCA ATTATGTTGC 2630
ACGTACACTC ATTGTACAGG CGTGGAGACT CATTGTATGT ATAAGAATAT TCTGACAGTG 2690
AGTGACCCGG AGTCTCTGGT GTACCCTCTT ACCAGTCAGC TGCCTGCGAG CAGTCATTTT 2750
TTCCTAAAGG TTTACAAGTA TTTAGAACTC TTCAGTTCAG GGCAAAATGT TCATGAAGTT 2810
ATTCTCTTA AACATGGTTA GGAAGCTGAT GACGTTATTG ATTTTGTCTG GATTATGTTT 2870
10 CTGGAATAAT TTTACCAAAA CAAGCTATTT GAGTTTTGAC TTGACAAGGC AAAACATGAC 2930
AGTGGATTCT CTTTACAAAT TGAACAAAAA AATCCTTATT TTGTATAAAG GACTTCCCTT 2990
TTTGTAAGT AATCCTTTTT ATTGGTAAAA ATTGTAAATT AAAATGTGCA ACTTG 3045

15 (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Epidermoid carcinoma

(C) CELL LINE: KB

(D) CLONE NAME: HP10389

(ix) SEQUENCE CHARACTERISTICS:

30 (A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 63.. 383

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

35

ATGACCTTCA CCGGGAGGCT GAGGTCGGAG TCCCGATTTT CTCCTGCTGC TGTGGCCCGG 60

AC ATG GCG ACT CCC GGC CCT GTG ATT CCG GAG GTC CCC TTT GAA CCA 107

Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro

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	1	5	10	15	
	TCG AAG CCT CCA GTC ATT GAG GGG CTG AGC CCC ACT GTT TAC AGG AAT				155
	Ser Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn				
		20	25	30	
5	CCA GAG AGT TTC AAG GAA AAG TTC GTT CGC AAG ACC CGC GAG AAC CCG				203
	Pro Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro				
		35	40	45	
	GTG GTA CCC ATA GGT TGC CTG GCC ACG GCG GCC GCC CTC ACC TAC GGC				251
	Val Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly				
10		50	55	60	
	CTC TAC TCC TTC CAC CGG GGC AAC AGC CAG CGC TCT CAG CTC ATG ATG				299
	Leu Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met				
		65	70	75	
	CGC ACC CGG ATC GCC GCC CAG GGT TTC ACG GTC GCA GCC ATC TTG CTG				347
15	Arg Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu				
		80	85	90	95
	GGT CTG GCT GTC ACT GCT ATG AAG TCT CGA CCC TAAGCCCAGG GTCTGGCCTT				400
	Gly Leu Ala Val Thr Ala Met Lys Ser Arg Pro				
		100	105		
20	GAAAGCTCCG CAGAAATGAT TCCAAAACCC AGGGAGCAAC CACTGGCCCT ACCGTGGGAC				460
	TTACTCCCTC CTCTCCTTTG AGAGGCCCAT GTGTGCTGG GGAGGAAGTG ACCCTTTGTG				520
	TAAGTGTAA CAGAAAGTTTT TTCAAAAATC CTAGATGCTG TTGTTTGAAT GTTACATACT				580
	TCTATTTGTG CCACATCTCC CCTCCACTCC CCTGCTTAAT AAAGTCTAAA AATCCACTTG				640
	TATTTAATTC AGT				653
25					

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10408

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(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
 (B) EXISTENCE POSITION: 75.. 311
 (C) CHARACTERIZATION METHOD: E

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GTAGAAACAG GCCTGTTAAG GAGAGGCCAC CGGGACTTCA GTGTCTCCTC CATCCCAGGA 60
 GCGCAGTGGC CACT ATG GGG TCT GGG CTG CCC CTT GTC CTC CTC TTG ACC 110
 10 Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr
 1 5 10
 CTC CTT GGC AGC TCA CAT GGA ACA GGG CCG GGT ATG ACT TTG CAA CTG 158
 Leu Leu Gly Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu
 15 20 25
 15 AAG CTG AAG GAG TCT TTT CTG ACA AAT TCC TCC TAT GAG TCC AGC TTC 206
 Lys Leu Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe
 30 35 40
 CTG GAA TTG CTT GAA AAG CTC TGC CTC CTC CTC CAT CTC CCT TCA GGG 254
 Leu Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
 20 45 50 55 60
 ACC AGC GTC ACC CTC CAC CAT GCA AGA TCT CAA CAC CAT GTT GTC TGC 302
 Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val Cys
 65 70 75
 AAC ACA TGACAGCCAT TGAAGCCTGT GTCCTTCTTG GCCCGGGCTT TTGGGCCGGG GA 360
 25 Asn Thr

 TGCAGGAGGC AGGCCCCGAC CCTGTCTTTC AGCAGGCCCC CACCCTCCTG AGTGGCAATA 420
 AATAAAATTC GGTATGCTG 439

30

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) SEQUENCE KIND: cDNA to mRNA

136

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 (D) CLONE NAME: HP10412

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(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
 (B) EXISTENCE POSITION: 56.. 1000
 (C) CHARACTERIZATION METHOD: E

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

	CTATGAGATC CCGGCCTCAG GGTGGACGCA GTGGTTCTGC ACTGAGGCCC TCGTC ATG	58
		Met
15		1
	GTG GCG CCT GTG TGG TAC TTG GTA GCG GCG GCT CTG CTA GTC GGC TTT	106
	Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe	
	5 10 15	
	ATC CTC TTC CTG ACT CGC AGC CGG GGC CGG GCG GCA TCA GCC GGC CAA	154
20	Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln	
	20 25 30	
	GAG CCA CTG CAC AAT GAG GAG CTG GCA GGA GCA GGC CGG GTG GCC CAG	202
	Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala Gln	
	35 40 45	
25	CCT GGG CCC CTG GAG CCT GAG GAG CCG AGA GCT GGA GGC AGG CCT CGG	250
	Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro Arg	
	50 55 60 65	
	CGC CGG AGG GAC CTG GGC AGC CGC CTA CAG GCC CAG CGT CGA GCC CAG	298
	Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala Gln	
30	70 75 80	
	CGG GTG GCC TGG GCA GAA GCA GAT GAG AAC GAG GAG GAA GCT GTC ATC	346
	Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val Ile	
	85 90 95	
	CTA GCC CAG GAG GAG GAA GGT GTC GAG AAG CCA GCG GAA ACT CAC CTG	394
35	Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His Leu	
	100 105 110	
	TCG GGG AAA ATT GGA GCT AAG AAA CTG CGG AAG CTG GAG GAG AAA CAA	442
	Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys Gln	

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	115	120	125	
	CGC CGA AAG GCC CAG CGT GAG GCA GAG GAG GCT GAA CGT GAG GAG CGG			490
	Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu Arg			
	130	135	140	145
5	AAA CGA CTC GAG TCC CAG CGC GAA GCT GAG TGG AAG AAG GAG GAG GAG			538
	Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu Glu			
	150	155	160	
	CGG CTT CGC CTG GAG GAG GAG CAG AAG GAG GAG GAG GAG AGG AAG GCC			586
	Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys Ala			
10	165	170	175	
	CGC GAG GAG CAG GCC CAG CGG GAG CAT GAG GAG TAC CTG AAA CTG AAG			634
	Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu Lys			
	180	185	190	
	GAG GCC TTT GTG GTG GAG GAG GAA GGC GTA GGA GAG ACC ATG ACT GAG			682
15	Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr Glu			
	195	200	205	
	GAA CAG TCC CAG AGC TTC CTG ACA GAG TTC ATC AAC TAC ATC AAG CAG			730
	Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys Gln			
	210	215	220	225
20	TCC AAG GTT GTG CTC TTG GAA GAC CTG GCT TCC CAG GTG GGC CTA CGC			778
	Ser Lys Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu Arg			
	230	235	240	
	ACT CAG GAC ACC ATA AAT CGC ATC CAG GAC CTG CTG GCT GAG GGG ACT			826
	Thr Gln Asp Thr Ile Asn Arg Ile Gln Asp Leu Leu Ala Glu Gly Thr			
25	245	250	255	
	ATA ACA GGT GTG ATT GAC GAC CGG GGC AAG TTC ATC TAC ATA ACC CCA			874
	Ile Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile Tyr Ile Thr Pro			
	260	265	270	
	GAG GAA CTG GCC GCC GTG GCC AAC TTC ATC CGA CAG CGG GGC CGG GTG			922
30	Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg Gln Arg Gly Arg Val			
	275	280	285	
	TCC ATC GCC GAG CTT GCC CAA GCC AGC AAC TCC CTC ATC GCC TGG GGC			970
	Ser Ile Ala Glu Leu Ala Gln Ala Ser Asn Ser Leu Ile Ala Trp Gly			
	290	295	300	305
35	CGG GAG TCC CCT GCC CAA GCC CCA GCC TGACCCAGT CCTCCCTCT TGG			1020
	Arg Glu Ser Pro Ala Gln Ala Pro Ala			
	310			
	ACTCAGAGTT GGTGTGGCCT ACCTGGCTAT ACATCTTCAT CCCTCCCCAC CATCCTGGGG			1080

AAGTGATGGT GTGGCCAGGC AGTTATAGAT TAAAGGCCCTG TGAGTACTGC T

1131

(2) INFORMATION FOR SEQ ID NO: 46:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1875

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

10 (ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

15 (D) CLONE NAME: HP10413

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 79.. 666

20 (C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

	CTCGCTCGCT CAGAGGGAGG AGAAAGTGGC GAGTTCCGGA TCCCTGCCTA GCGCGGCCCA	60
25	ACCTTTACTC CAGAGATC ATG GCT GCC GAG GAT GTG GTG GCG ACT GGC GCC	111
	Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala	
	1 5 10	
	GAC CCA AGC GAT CTG GAG AGC GGC GGG CTG CTG CAT GAG ATT TTC ACG	159
	Asp Pro Ser Asp Leu Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr	
30	15 20 25	
	TCG CCG CTC AAC CTG CTG CTG CTT GGC CTC TGC ATC TTC CTG CTC TAC	207
	Ser Pro Leu Asn Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr	
	30 35 40	
	AAG ATC GTG CGC GGC GAC CAG CCG GCG GCC AGC GGC GAC AGC GAC GAC	255
35	Lys Ile Val Arg Gly Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp	
	45 50 55	
	GAC GAG CCG CCC CCT CTG CCC CGC CTC AAG CGG CGC GAC TTC ACC CCC	303
	Asp Glu Pro Pro Pro Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro	

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	60	65	70	75	
	GCC GAG CTG CGG CGC TTC GAC GGC GTC CAG GAC CCG CGC ATA CTC ATG				351
	Ala Glu Leu Arg Arg Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met				
		80	85	90	
5	GCC ATC AAC GGC AAG GTG TTC GAT GTG ACC AAA GGC CGC AAA TTC TAC				399
	Ala Ile Asn Gly Lys Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr				
		95	100	105	
	GGG CCC GAG GGC CCG TAT GGC GTC TTT GCT GGA AGA GAT GCA TCC AGG				447
	Gly Pro Glu Gly Pro Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg				
10		110	115	120	
	GGC CTT GCC ACA TTT TGC CTG GAT AAG GAA GCA CTG AAG GAT GAG TAC				495
	Gly Leu Ala Thr Phe Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr				
		125	130	135	
	GAT GAC CTT TCT GAC CTC ACT GCT GCC CAG CAG GAG ACT CTG AGT GAC				543
15	Asp Asp Leu Ser Asp Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp				
		140	145	150	155
	TGG GAG TCT CAG TTC ACT TTC AAG TAT CAT CAC GTG GGC AAA CTG CTG				591
	Trp Glu Ser Gln Phe Thr Phe Lys Tyr His His Val Gly Lys Leu Leu				
		160	165	170	
20	AAG GAG GGG GAG GAG CCC ACT GTG TAC TCA GAT GAG GAA GAA CCA AAA				639
	Lys Glu Gly Glu Glu Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys				
		175	180	185	
	GAT GAG AGT GCC CGG AAA AAT GAT TAAAGCATTC AGTGAAGTA TATCTAT				690
	Asp Glu Ser Ala Arg Lys Asn Asp				
25		190	195		
	TTTTGTATTT TGCAAAATCA TTTGTAACAG TCCACTCTGT CTTTAAAACA TAGTGATTAC				750
	AATATTTAGA AAGTTTGTAG CACTTGCTAT AAGTTTTTTA TAACATCACT AGTGACACTA				810
	ATAAAATTAA CTTCTTAGAA TGCATGATGT GTTGTGTGT CACAAATCCA GAAAGTGAAC				870
	TGCAGTGCTG TAATACACAT GTTAATACTG TTTTCTTCT ATCTGTAGTT AGTACAGGAT				930
30	GAATTTAAAT GTGTTTTTCC TGAGAGACAA GGAAGACTTG GGTATTTCCC AAAACAGGTA				990
	AAAATCTTAA ATGTGCACCA AGAGCAAAGG ATCAACTTTT AGTCATGATG TTCTGTAAAG				1050
	ACAACAAATC CCTTTTTTTT TCTCAATTGA CTTAACTGCA TGATTTCTGT TTTATCTACC				1110
	TCTAAAGCAA ATCTGCAGTG TTCCAAAGAC TTTGGTATGG ATTAAGCGCT GTCCAGTAAC				1170
	AAAATGAAAT CTCAAAACAG AGCTCAGCTG CAAAAAGCA TATTTTCTGT GTTTCTGGAC				1230
35	TGCACTGTTG TCCTTGCCCT CACATAGACA CTCAGACACC CTCACAAACA CAGTAGTCTA				1290
	TAGTTAGGAT TAAATAGGA TCTGAACATT CAAAAGAAAG CTTTGAAAAA AAAGAGCTGG				1350
	CTGGCCTAAA AACCTAAATA TATGATGAAG ATTGTAGGAC TGTCTTCCCA AGCCCCATGT				1410
	TCATGGTGGG GCAATGGTTA TTTGGTTATT TTAACAATT GGTTACTCTC ATTTGAAATG				1470

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AGGGAGGGAC ATACAGAATA GGAACAGGTG TTTGCTCTCC TAAGAGCCTT CATGCACACC 1530
 CCTGAACCAC GAGGAAACAG TACAGTCGCT AGTCAAGTGG TTTTAAAGT AAAGTATATT 1590
 CATAAGGTAA CAGTTATTCT GTTGTTATAA AACTATACCC ACTGCAAAAG TAGTAGTCAA 1650
 GTGTCTAGGT CTTTGATATT GCTCTTTTGG TTAACACTAA GCTTAAGTAG ACTATACAGT 1710
 5 TGTATGAATT TGTAAGAGTA TATGAACACC TAGTGAGATT TCAAACCTGT AATTGTGGTT 1770
 AAATAGTCAT TGTATTTTCT TGTGAACCTGT GTTTTATGAT TTTACCTCAA ATCAGAAAAC 1830
 AAAATGATGT GCTTTGGTCA GTTAATAAAA ATGGTTTAC CCACT 1875

10 (2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1563

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

15 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

20 (B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10415

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

25 (B) EXISTENCE POSITION: 72.. 1460

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

30 AAATTGGGCC AGGCTGAGGC GCTGCTGCTG GAGCGGCCGA TCCGAGACGT GGCTCCCTGG 60
 GCGGCAGAAC C ATG TTG GAC TTC GCG ATC TTC GCC GTT ACC TTC TTG CTG 110
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu
 1 5 10
 GCG TTG GTG GGA GCC GTG CTC TAC CTC TAT CCG GCT TCC AGA CAA GCT 158
 35 Ala Leu Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala
 15 20 25
 GCA GGA ATT CCA GGG ATT ACT CCA ACT GAA GAA AAA GAT GGT AAT CTT 206
 Ala Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu

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	30	35	40	45	
	CCA GAT ATT GTG AAT AGT GGA AGT TTG CAT GAG TTC CTG GTT AAT TTG				254
	Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu				
	50	55	60		
5	CAT GAG AGA TAT GGG CCT GTG GTC TCC TTC TGG TTT GGC AGG CGC CTC				302
	His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu				
	65	70	75		
	GTG GTT AGT TTG GGC ACT GTT GAT GTA CTG AAG CAG CAT ATC AAT CCC				350
	Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro				
10	80	85	90		
	AAT AAG ACA TTG GAC CCT TTT GAA ACC ATG CTG AAG TCA TTA TTA AGG				398
	Asn Lys Thr Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg				
	95	100	105		
	TAT CAA TCT GGT GGT GGC AGT GTG AGT GAA AAC CAC ATG AGG AAA AAA				446
15	Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn His Met Arg Lys Lys				
	110	115	120	125	
	TTG TAT GAA AAT GGT GTG ACT GAT TCT CTG AAG AGT AAC TTT GCC CTC				494
	Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu Lys Ser Asn Phe Ala Leu				
	130	135	140		
20	CTC CTA AAG CTT TCA GAA GAA TTA TTA GAT AAA TGG CTC TCC TAC CCA				542
	Leu Leu Lys Leu Ser Glu Glu Leu Leu Asp Lys Trp Leu Ser Tyr Pro				
	145	150	155		
	GAG ACC CAG CAC GTG CCC CTC AGC CAG CAT ATG CTT GGT TTT GCT ATG				590
	Glu Thr Gln His Val Pro Leu Ser Gln His Met Leu Gly Phe Ala Met				
25	160	165	170		
	AAG TCT GTT ACA CAG ATG GTA ATG GGT AGT ACA TTT GAA GAT GAT CAG				638
	Lys Ser Val Thr Gln Met Val Met Gly Ser Thr Phe Glu Asp Asp Gln				
	175	180	185		
	GAA GTC ATT CGC TTC CAG AAG AAT CAT GGC ACA GTT TGG TCT GAG ATT				686
30	Glu Val Ile Arg Phe Gln Lys Asn His Gly Thr Val Trp Ser Glu Ile				
	190	195	200	205	
	GGA AAA GGC TTT CTA GAT GGG TCA CTT GAT AAA AAC ATG ACT CGG AAA				734
	Gly Lys Gly Phe Leu Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys				
	210	215	220		
35	AAA CAA TAT GAA GAT GCC CTC ATG CAA CTG GAG TCT GTT TTA AGG AAC				782
	Lys Gln Tyr Glu Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn				
	225	230	235		
	ATC ATA AAA GAA CGA AAA GGA AGG AAC TTC AGT CAA CAT ATT TTC ATT				830

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	Ile	Ile	Lys	Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	
	240					245					250						
	GAC	TCC	TTA	GTA	CAA	GGG	AAC	CTT	AAT	GAC	CAA	CAG	ATC	CTA	GAA	GAC	878
	Asp	Ser	Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	
5	255					260					265						
	AGT	ATG	ATA	TTT	TCT	CTG	GCC	AGT	TGC	ATA	ATA	ACT	GCA	AAA	TTG	TGT	926
	Ser	Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	
	270					275					280					285	
	ACC	TGG	GCA	ATC	TGT	TTT	TTA	ACC	ACC	TCT	GAA	GAA	GTT	CAA	AAA	AAA	974
10	Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys	
	290					295					300						
	TTA	TAT	GAA	GAG	ATA	AAC	CAA	GTT	TTT	GGA	AAT	GGT	CCT	GTT	ACT	CCA	1022
	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	Thr	Pro	
	305					310					315						
15	GAG	AAA	ATT	GAG	CAG	CTC	AGA	TAT	TGT	CAG	CAT	GTG	CTT	TGT	GAA	ACT	1070
	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	Cys	Glu	Thr	
	320					325					330						
	GTT	CGA	ACT	GCC	AAA	CTG	ACT	CCA	GTT	TCT	GCC	CAG	CTT	CAA	GAT	ATT	1118
	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	Leu	Gln	Asp	Ile	
20	335					340					345						
	GAA	GGA	AAA	ATT	GAC	CGA	TTT	ATT	ATT	CCT	AGA	GAG	ACC	CTC	GTC	CTT	1166
	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	Glu	Thr	Leu	Val	Leu	
	350					355					360					365	
	TAT	GCC	CTT	GGT	GTG	GTA	CTT	CAG	GAT	CCT	AAT	ACT	TGG	CCA	TCT	CCA	1214
25	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	Asn	Thr	Trp	Pro	Ser	Pro	
	370					375					380						
	CAC	AAG	TTT	GAT	CCA	GAT	CGG	TTT	GAT	GAT	GAA	TTA	GTA	ATG	AAA	ACT	1262
	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	Asp	Glu	Leu	Val	Met	Lys	Thr	
	385					390					395						
30	TTT	TCC	TCA	CTT	GGA	TTC	TCA	GGC	ACA	CAG	GAG	TGT	CCA	GAG	TTG	AGG	1310
	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	
	400					405					410						
	TTT	GCA	TAT	ATG	GTG	ACC	ACA	GTA	CTT	CTT	AGT	GTA	TTG	GTG	AAG	AGA	1358
	Phe	Ala	Tyr	Met	Val	Thr	Thr	Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	
35	415					420					425						
	CTG	CAC	CTA	CTT	TCT	GTG	GAG	GGA	CAG	GTT	ATT	GAA	ACA	AAG	TAT	GAA	1406
	Leu	His	Leu	Leu	Ser	Val	Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	
	430					435					440					445	

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CTG GTA ACA TCA TCA AGG GAA GAA GCT TGG ATC ACT GTC TCA AAG AGA 1454
 Leu Val Thr Ser Ser Arg Glu Glu Ala Trp Ile Thr Val S r Lys Arg
 450 455 460

TAT TAAAATTTTA TACATTTAAA ATCATTGTGA AATTGATTGA GGAAAACAAC CAT 1510

5 Tyr

TTAAAAA TCTATGTTGA ATCCTTTTAT AAACCAGTAT CACTTTGTAA TAT 1563

10 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2030

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

15 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

20 (B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10419

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

25 (B) EXISTENCE POSITION: 171.. 914

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

30 CATTTGGGGT TTCGGTCCG CCCCTTCCCC TTCCCCGGGG TCTGGGGGTG ACATTGCACC 60

GCGCCCCCTCG TGGGGTCGCG TTGCCACCCC ACGCGGACTC CCCAGCTGGC GCGCCCCCTCC 120

CATTTGCCTG TCCTGGTCAG GCCCCACCC CCCTTCCCAC CTGACCAGCC ATG GGG 176

Met Gly

1

35 GCT GCG GTG TTT TTC GGC TGC ACT TTC GTC GCG TTC GGC CCG GCC TTC 224

Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro Ala Phe

5

10

15

GCG CTT TTC TTG ATC ACT GTG GCT GGG GAC CCG CTT CGC GTT ATC ATC 272

144

	Ala	Leu	Phe	Leu	Ile	Thr	Val	Ala	Gly	Asp	Pro	L	u	Arg	Val	Ile	Ile	
	20						25					30						
	CTG	GTC	GCA	GGG	GCA	TTT	TTC	TGG	CTG	GTC	TCC	CTG	CTC	CTG	GCC	TCT		320
	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	Leu	Leu	Leu	Ala	Ser		
5	35					40					45					50		
	GTG	GTC	TGG	TTC	ATC	TTG	GTC	CAT	GTG	ACC	GAC	CGG	TCA	GAT	GCC	CGG		368
	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	Asp	Arg	Ser	Asp	Ala	Arg		
					55					60					65			
	CTC	CAG	TAC	GGC	CTC	CTG	ATT	TTT	GGT	GCT	GCT	GTC	TCT	GTC	CTT	CTA		416
10	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	Ala	Ala	Val	Ser	Val	Leu	Leu		
		70							75					80				
	CAG	GAG	GTG	TTC	CGC	TTT	GCC	TAC	TAC	AAG	CTG	CTT	AAG	AAG	GCA	GAT		464
	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Asp		
		85						90					95					
15	GAG	GGG	TTA	GCA	TCG	CTG	AGT	GAG	GAC	GGA	AGA	TCA	CCC	ATC	TCC	ATC		512
	Glu	Gly	Leu	Ala	Ser	Leu	Ser	Glu	Asp	Gly	Arg	Ser	Pro	Ile	Ser	Ile		
		100					105					110						
	CGC	CAG	ATG	GCC	TAT	GTT	TCT	GGT	CTC	TCC	TTC	GGT	ATC	ATC	AGT	GGT		560
	Arg	Gln	Met	Ala	Tyr	Val	Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile	Ser	Gly		
20	115					120				125					130			
	GTC	TTC	TCT	GTT	ATC	AAT	ATT	TTG	GCT	GAT	GCA	CTT	GGG	CCA	GGT	GTG		608
	Val	Phe	Ser	Val	Ile	Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro	Gly	Val		
					135					140					145			
	GTT	GGG	ATC	CAT	GGA	GAC	TCA	CCC	TAT	TAC	TTC	CTG	ACT	TCA	GCC	TTT		656
25	Val	Gly	Ile	His	Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser	Ala	Phe		
				150					155					160				
	CTG	ACA	GCA	GCC	ATT	ATC	CTG	CTC	CAT	ACC	TTT	TGG	GGA	GTT	GTG	TTC		704
	Leu	Thr	Ala	Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val	Val	Phe		
		165					170					175						
30	TTT	GAT	GCC	TGT	GAG	AGG	AGA	CGG	TAC	TGG	GCT	TTG	GGC	CTG	GTG	GTT		752
	Phe	Asp	Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu	Val	Val		
		180				185						190						
	GGG	AGT	CAC	CTA	CTG	ACA	TCG	GGA	CTG	ACA	TTC	CTG	AAC	CCC	TGG	TAT		800
	Gly	Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro	Trp	Tyr		
35	195					200				205					210			
	GAG	GCC	AGC	CTG	CTG	CCC	ATC	TAT	GCA	GTC	ACT	GTT	TCC	ATG	GGG	CTC		848
	Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met	Gly	Leu		
					215					220					225			

145

TGG GCC TTC ATC ACA GCT GGA GGG TCC CTC CGA AGT ATT CAG CGC AGC 896
Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln Arg Ser
230 235 240
CTC TTG TGT AAG GAC TGA CTACCTG GACTGATCGC CTGACAGATC CCACCTGCC 950
5 Leu Leu Cys Lys Asp
245
TGTCCACTGC CCATGACTGA GCCCAGCCCC AGCCCGGGTC CATTGCCCAC ATTCTCTGTC 1010
TCCTTCTCGT CGGTCTACCC CACTACCTCC AGGGTTTTGC TTTGTCTTT TGTGACCGTT 1070
AGTCTCTAAG CTTTACCAGG AGCAGCCTGG GTTCAGCCAG TCAGTGACTG GTGGGTTTGA 1130
10 ATCTGCACTT ATCCCCACCA CCTGGGGACC CCCTTGTTGT GTCCAGGACT CCCCTGTGT 1190
CAGTGCTCTG CTCTACCCCT GCCCAAGACT CACCTCCCTT CCCCTCTGCA GGCCGACGGC 1250
AGGAGGACAG TCGGGTGATG GTGTATTCTG CCCTGCGCAT CCCACCCGAG GACTGAGGGA 1310
ACCTAGGGGG GACCCCTGGG CCTGGGGTGC CCTCCTGATG TCCTCGCCCT GTATTTCTCC 1370
ATCTCCAGTT CTGGACAGTG CAGGTTGCCA AGAAAAGGGA CCTAGTTTAG CCATTGCCCT 1430
15 GGAGATGAAA TTAATGGAGG CTCAAGGATA GATGAGCTCT GAGTTTCTCA GTACTCCCTC 1490
AAGACTGGAC ATCTTGGTCT TTTTCTCAGG CCTGAGGGGG AACCATTTTT GGTGTGATAA 1550
ATACCTAAA CTGCCTTTTT TTCTTTTTTG AGGTGGGGGG AGGGAGGAGG TATATTGGAA 1610
CTCTTCTAAC CTCCTTGGGC TATATTTTCT CTCCTCGAGT TGCTCCTCAT GGCTGGGCTC 1670
ATTCGGTCC CTTTCTCCTT GGTCCCAGAC CTGGGGGAA AGGAAGGAAG TGCATGTTTG 1730
20 GGAAGTGGCA TTAAGTGAAC TAATGGTTTT AACCTCCTTA ACCACCAGCA TCCCTCCTCT 1790
CCCCAAGGTG AAGTGGAGGG TGCTGTGGTG AGCTGGCCAC TCCAGAGCTG CAGTGCCACT 1850
GGAGGAGTCA GACTACCATG ACATCGTAGG GAAGGAGGGG AGATTTTTTT GTAGTTTTTA 1910
ATTGGGGTGT GGGAGGGGCG GGGAGGTTTT CTATAAACTG TATCATTTTC TGCTGAGGGT 1970
GGAGTGTCCT ATCCTTTTAA TCAAGGTGAT TGTGATTTTG ACTAATAAAA AAGAATTTGT 2030
25

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10424

146

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
 (B) EXISTENCE POSITION: 98.. 439
 (C) CHARACTERIZATION METHOD: E

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AAAGTTTCCC AAATCCAGGC GGCTAGAGGC CCACTGCTTC CCAACTACCA GCTGAGGGGG 60
 TCCGTCCCGA GAAGGGAGAA GAGGCCGAAG AGGAAAC ATG AAC TTC TAT TTA CTC 115
 10 Met Asn Phe Tyr Leu Leu
 1 5
 CTA GCG AGC AGC ATT CTG TGT GCC TTG ATT GTC TTC TGG AAA TAT CGC 163
 Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile Val Phe Trp Lys Tyr Arg
 10 15 20
 15 CGC TTT CAG AGA AAC ACT GGC GAA ATG TCA TCA AAT TCA ACT GCT CTT 211
 Arg Phe Gln Arg Asn Thr Gly Glu Met Ser Ser Asn Ser Thr Ala Leu
 25 30 35
 GCA CTA GTG AGA CCC TCT TCT TCT GGG TTA ATT AAC AGC AAT ACA GAC 259
 Ala Leu Val Arg Pro Ser Ser Ser Gly Leu Ile Asn Ser Asn Thr Asp
 20 40 45 50
 AAC AAT CTT GCA GTC TAC GAC CTC TCT CGG GAT ATT TTA AAT AAT TTC 307
 Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg Asp Ile Leu Asn Asn Phe
 55 60 65 70
 CCA CAC TCA ATA GCC AGG CAG AAG CGA ATA TTG GTA AAC CTC AGT ATG 355
 25 Pro His Ser Ile Ala Arg Gln Lys Arg Ile Leu Val Asn Leu Ser Met
 75 80 85
 GTG GAA AAC AAG CTG GTT GAA CTG GAA CAT ACT CTA CTT AGC AAG GGT 403
 Val Glu Asn Lys Leu Val Glu Leu Glu His Thr Leu Leu Ser Lys Gly
 90 95 100
 30 TTC AGA GGT GCA TCA CCT CAC CGG AAA TCC ACC TAAAAGCGTA CAGG 450
 Phe Arg Gly Ala Ser Pro His Arg Lys Ser Thr
 105 110
 ATGTAATGCC AGTGGTGGA ATCATTAAG ACACITTTGA GTAG 493

35

(2) INFORMATION FOR SEQ ID NO: 50:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2044

147

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Epidermoid carcinoma

(C) CELL LINE: KB

10

(D) CLONE NAME: HP10428

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 288.. 1385

15

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

	AGATTCCGGC CTGGAGCTCC CAGGGCCGAG CAGACCTTGG GACCTGTGAG CGCTGCATCC	60
20	AATTAACCAT GGGAAGGGTC AGCACCAGCC ACCAGCCCCT TAGGTGAGGA CTCTGCCTGG	120
	GGCTCTGCTG ATGGTTCCGA ATCATGGAGC TGCAGAGAGC TCCTCCAGCC TGGAGACGTT	180
	CTTGGTGAAA GCTGTGGTCT AACTCCACCG GCTCTTCCTG CACATTGTAT TCAAGAGGGG	240
	TGCCTGCCCC CGCTGACTCA GGAGCTCCGG TGCTGCAGCC GCCACGA ATG GGG AGG	296
		Met Gly Arg
25		1
	TGG GCC CTC GAT GTG GCC TTT TTG TGG AAG GCG GTG TTG ACC CTG GGG	344
	Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu Thr Leu Gly	
	5 10 15	
	CTG GTG CTT CTC TAC TAC TGC TTC TCC ATC GGC ATC ACC TTC TAC AAC	392
30	Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr Phe Tyr Asn	
	20 25 30 35	
	AAG TGG CTG ACA AAG AGC TTC CAT TTC CCC CTC TTC ATG ACG ATG CTG	440
	Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met Thr Met Leu	
	40 45 50	
35	CAC CTG GCC GTG ATC TTC CTC TTC TCC GCC CTG TCC AGG GCG CTG GTT	488
	His Leu Ala Val Ile Ph Leu Phe Ser Ala Leu Ser Arg Ala Leu Val	
	55 60 65	
	CAG TGC TCC AGC CAC AGG GCC CGT GTG GTG CTG AGC TGG GCC GAC TAC	536

148

	Gln	Cys	Ser	Ser	His	Arg	Ala	Arg	Val	Val	Leu	Ser	Trp	Ala	Asp	Tyr	
	70					75					80						
	CTC	AGA	AGA	GTG	GCT	CCC	ACA	GCT	CTG	GCG	ACG	GCG	CTT	GAC	GTG	GGC	584
	Leu	Arg	Arg	Val	Ala	Pro	Thr	Ala	Leu	Ala	Thr	Ala	Leu	Asp	Val	Gly	
5	85					90					95						
	TTG	TCC	AAC	TGG	AGC	TTC	CTG	TAT	GTC	ACC	GTC	TCG	CTG	TAC	ACA	ATG	632
	Leu	Ser	Asn	Trp	Ser	Phe	Leu	Tyr	Val	Thr	Val	Ser	Leu	Tyr	Thr	Met	
	100					105					110					115	
	ACC	AAA	TCC	TCA	GCT	GTC	CTC	TTC	ATC	TTG	ATC	TTC	TCT	CTG	ATC	TTC	680
10	Thr	Lys	Ser	Ser	Ala	Val	Leu	Phe	Ile	Leu	Ile	Phe	Ser	Leu	Ile	Phe	
	120					125					130						
	AAG	CTG	GAG	GAG	CTG	CGC	GCG	GCA	CTG	GTC	CTG	GTG	GTC	CTC	CTC	ATC	728
	Lys	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Val	Leu	Val	Val	Leu	Leu	Ile	
	135					140					145						
15	GCC	GGG	GGT	CTC	TTC	ATG	TTC	ACC	TAC	AAG	TCC	ACA	CAG	TTC	AAC	GTG	776
	Ala	Gly	Gly	Leu	Phe	Met	Phe	Thr	Tyr	Lys	Ser	Thr	Gln	Phe	Asn	Val	
	150					155					160						
	GAG	GGC	TTC	GCC	TTG	GTG	CTG	GGG	GCC	TCG	TTC	ATC	GGT	GGC	ATT	CGC	824
	Glu	Gly	Phe	Ala	Leu	Val	Leu	Gly	Ala	Ser	Phe	Ile	Gly	Gly	Ile	Arg	
20	165					170					175						
	TGG	ACC	CTC	ACC	CAG	ATG	CTC	CTG	CAG	AAG	GCT	GAA	CTC	GGC	CTC	CAG	872
	Trp	Thr	Leu	Thr	Gln	Met	Leu	Leu	Gln	Lys	Ala	Glu	Leu	Gly	Leu	Gln	
	180					185					190					195	
	AAT	CCC	ATC	GAC	ACC	ATG	TTC	CAC	CTG	CAG	CCA	CTC	ATG	TTC	CTG	GGG	920
25	Asn	Pro	Ile	Asp	Thr	Met	Phe	His	Leu	Gln	Pro	Leu	Met	Phe	Leu	Gly	
	200					205					210						
	CTC	TTC	CCT	CTC	TTT	GCT	GTA	TTT	GAA	GGT	CTC	CAT	TTG	TCC	ACA	TCT	968
	Leu	Phe	Pro	Leu	Phe	Ala	Val	Phe	Glu	Gly	Leu	His	Leu	Ser	Thr	Ser	
	215					220					225						
30	GAG	AAA	ATC	TTC	CGT	TTC	CAG	GAC	ACA	GGG	CTG	CTC	CTG	CGG	GTA	CTT	1016
	Glu	Lys	Ile	Phe	Arg	Phe	Gln	Asp	Thr	Gly	Leu	Leu	Leu	Arg	Val	Leu	
	230					235					240						
	GGG	AGC	CTC	TTC	CTT	GGC	GGG	ATT	CTC	GCC	TTT	GGT	TTG	GGC	TTC	TCT	1064
	Gly	Ser	Leu	Phe	Leu	Gly	Gly	Ile	Leu	Ala	Phe	Gly	Leu	Gly	Phe	Ser	
35	245					250					255						
	GAG	TTC	CTC	CTG	GTC	TCC	AGA	ACC	TCC	AGC	CTC	ACT	CTC	TCC	ATT	GCC	1112
	Glu	Phe	Leu	Leu	Val	Ser	Arg	Thr	Ser	Ser	Leu	Thr	Leu	Ser	Il	Ala	
	260					265					270					275	

149

GGC ATT TTT AAG GAA GTC TGC ACT TTG CTG TTG GCA GCT CAT CTG CTG 1160
 Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala His Leu Leu
 280 285 290
 GGC GAT CAG ATC AGC CTC CTG AAC TGG CTG GGC TTC GCC CTC TGC CTC 1208
 5 Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala Leu Cys Leu
 295 300 305
 TCG GGA ATA TCC CTC CAC GTT GCC CTC AAA GCC CTG CAT TCC AGA GGT 1256
 Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His Ser Arg Gly
 310 315 320
 10 GAT GGT GGC CCC AAG GCC TTG AAG GGG CTG GGC TCC AGC CCC GAC CTG 1304
 Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser Pro Asp Leu
 325 330 335
 GAG CTG CTG CTC CGG AGC AGC CAG CGG GAG GAA GGT GAC AAT GAG GAG 1352
 Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp Asn Glu Glu
 15 340 345 350 355
 GAG GAG TAC TTT GTG GCC CAG GGG CAG CAG TGACCAGCCA GGGCAAAT 1400
 Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln
 360 365
 GGCTTAGAAG CAGGCCACTC CCCAGCCTGC TGCCAGCACT CACTGTGCTC AAGCCGCCAG 1460
 20 GGCTCATCAT GGTAGCTGGG AGCTGTGGAC GGGAGTCACC AGGTGGTGGG GCCAAGCCAG 1520
 GGA CTG CAT GAA CTT TTT G CCCC TCC CTT CAGA GCCTGGTCAC ACAAGGGGCG AGCACCAGGC 1580
 CAGCCTGGGA CTGGCCAGAG CTGGGCCCAA GCTGCGCTGG AATCGCAGCA GGAGAGGGGA 1640
 GTGGGCTGGT TCTTCCCACC ACTTCCCAGG CTCTGACAGC CGAGACTCAT TTCCAAGGCA 1700
 CAGCAGCTTT CTAAAGGGAC TGAGTTTGGG CTGGGTTTTG GACCTCCAGG GGCTGGAGCT 1760
 25 TCATCACCTG GGCAGTGTCT TTTCTCAGAG AGCAGGTTTC TTTATAGTTT GGAAATAAAT 1820
 GGTTACGGT CCACTGGCCG CCTTGTGTTG CTGGAGACGT GGGGGCAGGG AGGGGACAGT 1880
 GTGGGCCTGG CCTCTCCTTT CCTTCCCTG CCTGGAGCCT TCTTCAAATG TCTGGTCTTA 1940
 AGCCAGGCCT CCTTCATTTT CTCGCTCCTG TTAGAACACC AGTCCCCTCC CCAGTGGGGC 2000
 CCCACTGCAC CTGCTGGCAG GAAATAAATG AATGTTTACT GAGT 2044
 30

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1043

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

150

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 (D) CLONE NAME: HP10429

5

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
 (B) EXISTENCE POSITION: 157.. 837
 (C) CHARACTERIZATION METHOD: E

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

	ATTAGCATAA CCCTTCCTCA GGAAGAGTGA GATTTTATAT TTGACAATAA AGTGTTAGAC	60
	TCCATTTCTA AATACCAGAC TTCAAAAGAT AAGGTTCAAA AGTGTTATAA GAAGATATTC	120
15	CTTTTTTGT CCTAGAGAAC TTATTTTCCT GTGAAA ATG CCT ACC ACA AAG AAG	174
	Met Pro Thr Thr Lys Lys	
	1 5	
	ACA TTG ATG TTC TTA TCA AGC TTT TTC ACC AGC CTT GGG TCC TTC ATT	222
	Thr Leu Met Phe Leu Ser Ser Phe Phe Thr Ser Leu Gly Ser Phe Ile	
20	10 15 20	
	GTA ATT TGC TCT ATT CTT GGG ACA CAA GCA TGG ATC ACC AGT ACA ATT	270
	Val Ile Cys Ser Ile Leu Gly Thr Gln Ala Trp Ile Thr Ser Thr Ile	
	25 30 35	
	GCT GTT AGA GAC TCT GCT TCA AAT GGG AGC ATT TTC ATC ACT TAC GGA	318
25	Ala Val Arg Asp Ser Ala Ser Asn Gly Ser Ile Phe Ile Thr Tyr Gly	
	40 45 50	
	CTT TTT CGT GGG GAG AGT AGT GAA GAA TTG AGT CAC GGA CTT GCA GAA	366
	Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu Ser His Gly Leu Ala Glu	
	55 60 65 70	
30	CCA AAG AAA AAG TTT GCA GTT TTA GAG ATA CTG AAT AAT TCT TCC CAA	414
	Pro Lys Lys Lys Phe Ala Val Leu Glu Ile Leu Asn Asn Ser Ser Gln	
	75 80 85	
	AAA ACT CTG CAT TCG GTG ACT ATC CTG TTC CTG GTC CTG AGT TTG ATC	462
	Lys Thr Leu His Ser Val Thr Ile Leu Phe Leu Val Leu Ser Leu Ile	
35	90 95 100	
	ACG TCG CTG CTG AGC TCT GGG TTT ACC TTC TAC AAC AGC ATC AGC AAC	510
	Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe Tyr Asn Ser Ile Ser Asn	
	105 110 115	

151

	CCT TAC CAG ACA TTC CTG GGG CCG ACG GGG GTG TAC ACC TGG AAC GGG	558
	Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly Val Tyr Thr Trp Asn Gly	
	120 125 130	
	CTC GGT GCA TCC TTC GTT TTT GTG ACC ATG ATA CTG TTT GTG GCG AAC	606
5	Leu Gly Ala Ser Phe Val Phe Val Thr Met Ile Leu Phe Val Ala Asn	
	135 140 145 150	
	ACG CAG TCC AAC CAA CTC TCC GAA GAG TTG TTC CAA ATG CTT TAC CCG	654
	Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu Phe Gln Met Leu Tyr Pro	
	155 160 165	
10	GCA ACC ACC AGT AAA GGA ACG ACC CAC AGT TAC GGA TAC TCG TTC TGG	702
	Ala Thr Thr Ser Lys Gly Thr Thr His Ser Tyr Gly Tyr Ser Phe Trp	
	170 175 180	
	CTC ATA CTG CTC GTC ATT CTT CTA AAT ATA GTC ACT GTA ACC ATC ATC	750
	Leu Ile Leu Leu Val Ile Leu Leu Asn Ile Val Thr Val Thr Ile Ile	
15	185 190 195	
	ATT TTC TAC CAG AAG GCC AGA TAC CAG CGG AAG CAG GAG CAG AGA AAG	798
	Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg Lys Gln Glu Gln Arg Lys	
	200 205 210	
	CCA ATG GAA TAT GCT CCA AGG GAC GGA ATT TTA TTC TGAATTCTCT TTCATC	850
20	Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile Leu Phe	
	215 220 225	
	TCATTTTGGC GTTGCATCTA TTGTACATCA GCCCTGAGTA GTAAGTGGTT AGCTTCTCTG	910
	GACAATTCAG CATGGTAACG TGAAGTGCAT CTGTGACAGC ATTTGTGTTT CATGACACTG	970
	TGTTCTTCAT TGATGCTGTA CTCCTGAAAA TTTTCCAC AAGGTTGGGG AAATGAATGG	1030
25	GAAATGTCGC TGG	1043

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 972

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

152

(D) CLONE NAME: HP10432

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

5 (B) EXISTENCE POSITION: 29.. 418

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

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10 AGACAGCGGC GGGCGCAGGA CGTGCACT ATG GCT CGG GGC TCG CTG CGC CGG      52
      Met Ala Arg Gly Ser Leu Arg Arg
      1              5
      TTG CTG CGG CTC CTC GTG CTG GGG CTC TGG CTG GCG TTG CTG CGC TCC      100
      Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
15      10              15              20
      GTG GCC GGG GAG CAA GCG CCA GGC ACC GCC CCC TGC TCC CGC GGC AGC      148
      Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
      25              30              35              40
      TCC TGG AGC GCG GAC CTG GAC AAG TGC ATG GAC TGC GCG TCT TGC AGG      196
20 Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
      45              50              55
      GCG CGA CCG CAC AGC GAC TTC TGC CTG GGC TGC GCT GCA GCA CCT CCT      244
      Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
      60              65              70
25 GCC CCC TTC CGG CTG CTT TGG CCC ATC CTT GGG GGC GCT CTG AGC CTG      292
      Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
      75              80              85
      ACC TTC GTG CTG GGG CTG CTT TCT GGC TTT TTG GTC TGG AGA CGA TGC      340
      Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
30      90              95              100
      CGC AGG AGA GAG AAG TTC ACC ACC CCC ATA GAG GAG ACC GGC GGA GAG      388
      Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
      105              110              115              120
      GGC TGC CCA GCT GTG GCG CTG ATC CAG TGACA ATGT GCCCCCTGCC A CCGG      440
35 Gly Cys Pro Ala Val Ala Leu Ile Gln
      125
      GGCTCGCCCA CTCATCATTC ATTCATCCAT TCTAGAGCCA GTCTCTGCCT CCCAGACGCG      500
      GCGGGAGCCA AGCTCCTCCA ACCACAAGGG GGGTGGGGGG CGGTGAATCA CCTCTGAGGC      560

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153

CTGGGCCCAG GGTTCAGGGG AACCTTCCAA GGTGTCTGGT TGCCCTGCCT CTGGCTCCAG 620
 AACAGAAAGG GAGCCTCACG CTGGCTCACA CAAAACAGCT GACACTGACT AAGGAACTGC 680
 AGCATTTGCA CAGGGGAGGG GGGTGCCCTC CTTCTAGAG GCCCTGGGGG CCAGGCTGAC 740
 TTGGGGGGCA GACTTGACAC TAGGCCCCAC TCACTCAGAT GTCCTGAAAT TCCACCACGG 800
 5 GGGTCACCCT GGGGGGTTAG GGACCTATTT TTAACACTAG GGGGCTGGCC CACTAGGAGG 860
 GCTGGCCCTA AGATACAGAC CCCCCCAACT CCCCAAAGCG GGGAGGAGAT ATTTATTTTG 920
 GGGAGAGTTT GGAGGGGAGG GAGAATTTAT TAATAAAGA ATCTTAACT TT 972

10 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 695

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

15 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

20 (B) CELL KIND: Liver

(C) CELL LINE:

(D) CLONE NAME: HP10433

(ix) SEQUENCE CHARACTERISTICS:

25 (A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 73.. 564

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

30

AAGATTTTCAG CTGCGGGACG GTCAGGGGAG ACCTCCAGGC GCAGGGAAGG ACGGCCAGGG 60

TGACACGGAA GC ATG CGA CGG CTG CTG ATC CCT CTG GCC CTG TGG CTG GGC 111

Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly

1

5

10

35 GCG GTG GGC GTG GGC GTC GCC GAG CTC ACG GAA GCC CAG CGC CGG GGC 159

Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly

15

20

25

CTG CAG GTG GCC CTG GAG GAA TTT CAC AAG CAC CCG CCC GTG CAG TGG 207

154

	Leu	Gln	Val	Ala	Leu	Glu	Glu	Phe	His	Lys	His	Pro	Pro	Val	Gln	Trp	
	30				35					40					45		
	GCC	TTC	CAG	GAG	ACC	AGT	GTG	GAG	AGC	GCC	GTG	GAC	ACG	CCC	TTC	CCA	255
	Ala	Phe	Gln	Glu	Thr	Ser	Val	Glu	Ser	Ala	Val	Asp	Thr	Pro	Phe	Pro	
5					50					55					60		
	GCT	GGA	ATA	TTT	GTG	AGG	CTG	GAA	TTT	AAG	CTG	CAG	CAG	ACA	AGC	TGC	303
	Ala	Gly	Ile	Phe	Val	Arg	Leu	Glu	Phe	Lys	Leu	Gln	Gln	Thr	Ser	Cys	
					65					70					75		
	CGG	AAG	AGG	GAC	TGG	AAG	AAA	CCC	GAG	TGC	AAA	GTC	AGG	CCC	AAT	GGG	351
10	Arg	Lys	Arg	Asp	Trp	Lys	Lys	Pro	Glu	Cys	Lys	Val	Arg	Pro	Asn	Gly	
		80						85					90				
	AGG	AAA	CGG	AAA	TGC	CTG	GCC	TGC	ATC	AAA	CTG	GGC	TCT	GAG	GAC	AAA	399
	Arg	Lys	Arg	Lys	Cys	Leu	Ala	Cys	Ile	Lys	Leu	Gly	Ser	Glu	Asp	Lys	
		95					100					105					
15	GTT	CTG	GGC	CGG	TTG	GTC	CAC	TGC	CCC	ATA	GAG	ACC	CAA	GTT	CTG	CGG	447
	Val	Leu	Gly	Arg	Leu	Val	His	Cys	Pro	Ile	Glu	Thr	Gln	Val	Leu	Arg	
		110				115				120					125		
	GAG	GCT	GAG	GAG	CAC	CAG	GAG	ACC	CAG	TGC	CTC	AGG	GTG	CAG	CGG	GCT	495
	Glu	Ala	Glu	Glu	His	Gln	Glu	Thr	Gln	Cys	Leu	Arg	Val	Gln	Arg	Ala	
20					130					135					140		
	GGT	GAG	GAC	CCC	CAC	AGC	TTC	TAC	TTC	CCT	GGA	CAG	TTC	GCC	TTC	TCC	543
	Gly	Glu	Asp	Pro	His	Ser	Phe	Tyr	Phe	Pro	Gly	Gln	Phe	Ala	Phe	Ser	
					145					150					155		
	AAG	GCC	CTG	CCC	CGC	AGC	TAAGCCAGCA	CTGAGCTGCG	TGGTGCCTC								590
25	Lys	Ala	Leu	Pro	Arg	Ser											
					160												
	CAGGACCGCT	GCCGGTGGTA	ACCACTGGAA	GACCCCAGCC	CCCAGGGAGA	GGACCCCGTT											650
	CTATCCCCAG	CCATGATAAT	AAAGCTGCTC	TCCCAGCTGC	CTCTC												695

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1914

(B) TYPE: Nucleic acid

35

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

155

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
 (B) CELL KIND: Stomach cancer
 (D) CLONE NAME: HP10480

5

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
 (B) EXISTENCE POSITION: 80.. 661
 (C) CHARACTERIZATION METHOD: E

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

	ACTCTCTGCT GTCGCCCCGTC CCGCGCGCTC CTCCGACCCG CTCCGCTCCG CTCCGCTCCG	60
	CCCCGCGCCG CCCGTCAAC ATG ATC CGC TGC GGC CTG GCC TGC GAG CGC TGC	112
15	Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys	
	1 5 10	
	CGC TGG ATC CTG CCC CTG CTC CTA CTC AGC GCC ATC GCC TTC GAC ATC	160
	Arg Trp Ile Leu Pro Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile	
	15 20 25	
20	ATC GCG CTG GCC GGC CGC GGC TGG TTG CAG TCT AGC GAC CAC GGC CAG	208
	Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln	
	30 35 40	
	ACG TCC TCG CTG TGG TGG AAA TGC TCC CAA GAG GGC GGC GGC AGC GGC	256
	Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly	
25	45 50 55	
	TCC TAC GAG GAG GGC TGT CAG AGC CTC ATG GAG TAC GCG TGG GGT AGA	304
	Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg	
	60 65 70 75	
	GCA GCG GCT GCC ATG CTC TTC TGT GGC TTC ATC ATC CTG GTG ATC TGT	352
30	Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys	
	80 85 90	
	TTC ATC CTC TCC TTC TTC GCC CTC TGT GGA CCC CAG ATG CTT GTC TTC	400
	Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe	
	95 100 105	
35	CTG AGA GTG ATT GGA GGT CTC CTT GCC TTG GCT GCT GTG TTC CAG ATC	448
	Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile	
	110 115 120	
	ATC TCC CTG GTA ATT TAC CCC GTG AAG TAC ACC CAG ACC TTC ACC CTT	496

156

	Ile Ser Leu Val Ile Tyr Pr Val Lys Tyr Thr Gln Thr Phe Thr Leu	
	125 130 135	
	CAT GCC AAC CGT GCT GTC ACT TAC ATC TAT AAC TGG GCC TAC GGC TTT	544
	His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe	
5	140 145 150 155	
	GGG TGG GCA GCC ACG ATT ATC CTG ATC GGC TGT GCC TTC TTC TTC TGC	592
	Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys	
	160 165 170	
	TGC CTC CCC AAC TAC GAA GAT GAC CTT CTG GGC AAT GCC AAG CCC AGG	640
10	Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg	
	175 180 185	
	TAC TTC TAC ACA TCT GCC TA ACTTGGG AATGAATGTG GGAGAAAATC GCT	690
	Tyr Phe Tyr Thr Ser Ala	
	190	
15	GCTGCTGAGA TGGACTCCAG AAGAAGAAAC TGTTTCTCCA GGCGACTTTG AACCCATTTT	750
	TTGGCAGTGT TCATATTATT AAAC TAGTCA AAAATGCTAA AATAATTTGG GAGAAAATAT	810
	TTTTTAAGTA GTGTTATAGT TTCATGTTTA TCTTTTATTA TGTTTTGTGA AGTTGTGTCT	870
	TTTCACTAAT TACCTATACT ATGCCAATAT TTCCTTATAT CTATCCATAA CATTTATACT	930
	ACATTTGTAA GAGAATATGC ACGTGAAACT TAACACTTTA TAAGGTAAAA ATGAGGTTTC	990
20	CAAGATTTAA TAATCTGATC AAGTTCTTGT TATTTCCAAA TAGAATGGAC TTGGTCTGTT	1050
	AAGGGCTAAG GAGAAGAGGA AGATAAGGTT AAAAGTTGTT AATGACCAAA CATTCTAAAA	1110
	GAAATGCAAA AAAAAAGTTT ATTTTCAAGC CTTCGAACTA TTAAAGGAAA GCAAAATCAT	1170
	TTCCTAAATG CATATCATTT GTGAGAATTT CTCATTAATA TCCTGAATCA TTCATTTTCTCAG	1230
	CTAAGGCTTC ATGTTGACTC GATATGTCAT CTAGGAAAGT ACTATTTTCAT GGTCCAAACC	1290
25	TGTTGCCATA GTTGTAAGG CTTTCCTTTA AGTGTGAAAT ATTTAGATGA AATTTTCTCT	1350
	TTTAAAGTTC TTTATAGGGT TAGGGTGTGG GAAAATGCTA TATTAATAAA TCTGTAGTGT	1410
	TTTGTGTTTA TATGTTTACA ACCAGAGTAG ACTGGATTGA AAGATGGACT GGGTCTAATT	1470
	TATCATGACT GATAGATCTG GTTAAGTTGT GTAGTAAAGC ATTAGGAGGG TCATTCTTGT	1530
	CACAAAAGTG CCACTAAAAC AGCCTCAGGA GAATAAATGA CTGCTTTTTC TAAATCTCAG	1590
30	GTTTATCTGG GCTCTATCAT ATAGACAGGC TTCTGATAGT TTGCAACTGT AAGCAGAAAC	1650
	CTACATATAG TTAAATCCT GGTCTTTCTT GGTAAACAGA TTTTAAATGT CTGATATAAA	1710
	ACATGCCACA GGAGAATTCG GGGATTTGAG TTTCTCTGAA TAGCATATAT ATGATGCATC	1770
	GGATAGGTCA TTATGATTTT TTACCATTTC GACTTACATA ATGAAAACCA ATTCATTTTA	1830
	AATATCAGAT TATTATTTTG TAAGTTGTGG AAAAAGCTAA TTGTAGTTTT CATTATGAAG	1890
35	TTTTCCCAAT AAACCAGGTA TTCT	1914

CLAIMS

1. A protein comprising an amino acid sequence selected
from the group consisting of the amino acid sequences of SEQ
5 ID NOS: 1 to 18.

2. A DNA encoding the protein according to claim 1.

3. A cDNA comprising a nucleotide sequence selected
10 from the group consisting of the nucleotide sequences of SEQ
ID NOS: 19 to 36.

4. A cDNA according to claim 3, which comprises a
nucleotide sequence selected from the group consisting of the
15 nucleotide sequences of SEQ ID NOS: 37 to 54.

5. An expression vector capable of in vitro translating
the DNA according to any of claims 2 to 4 or expressing said
DNA in an eukaryotic cell.

20

6. A transformed eukaryotic cell capable of expressing
the DNA according to any of claims 2 to 4 to produce the
protein according to claim 1.

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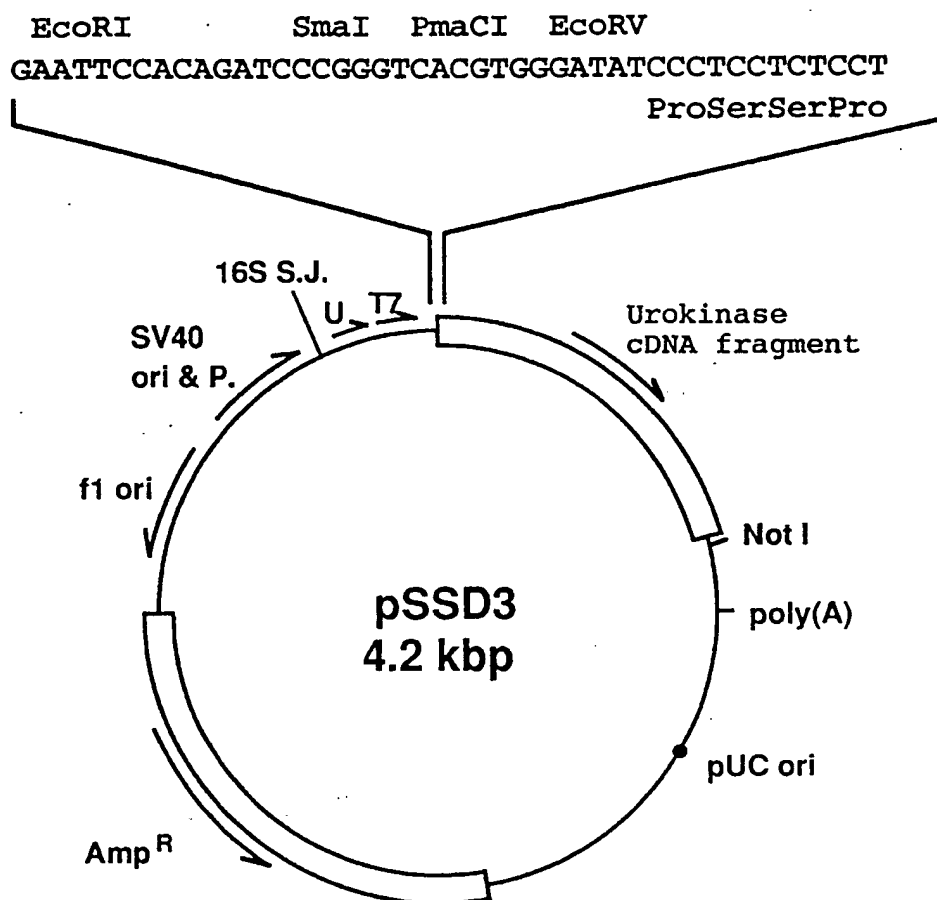


Fig.1

2/19

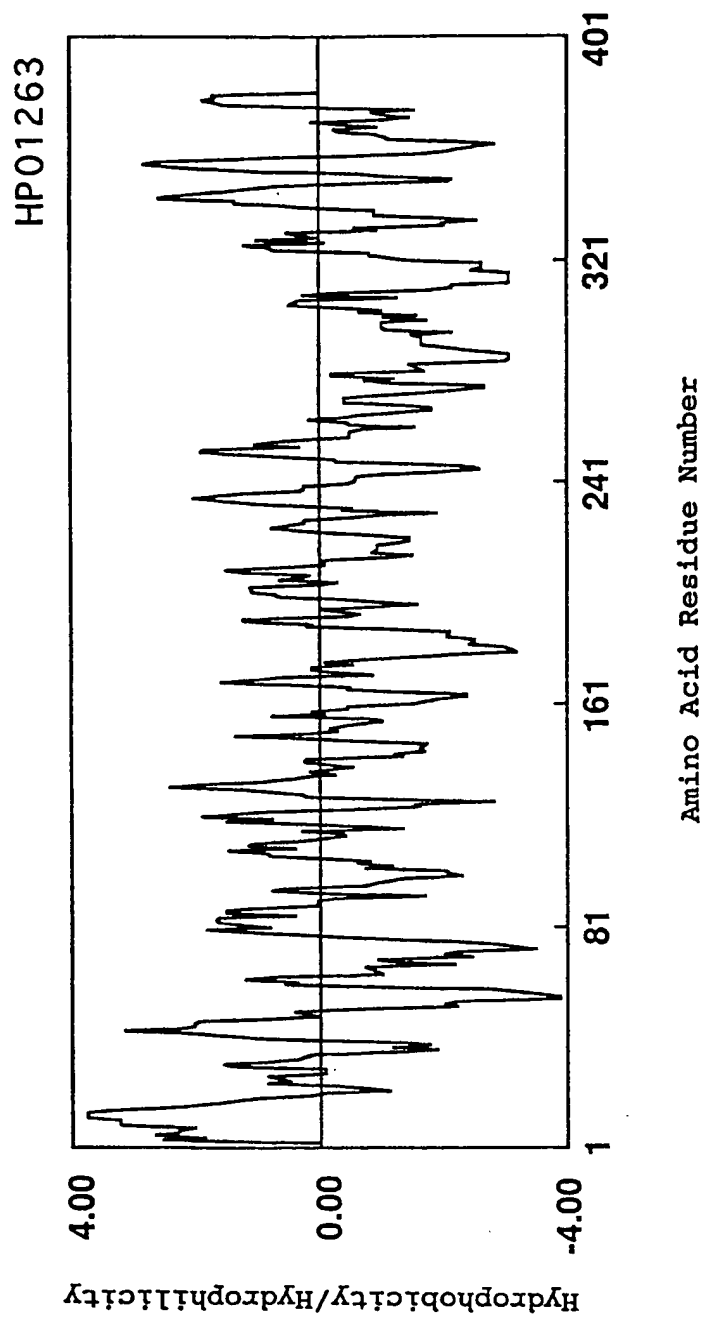


Fig.2

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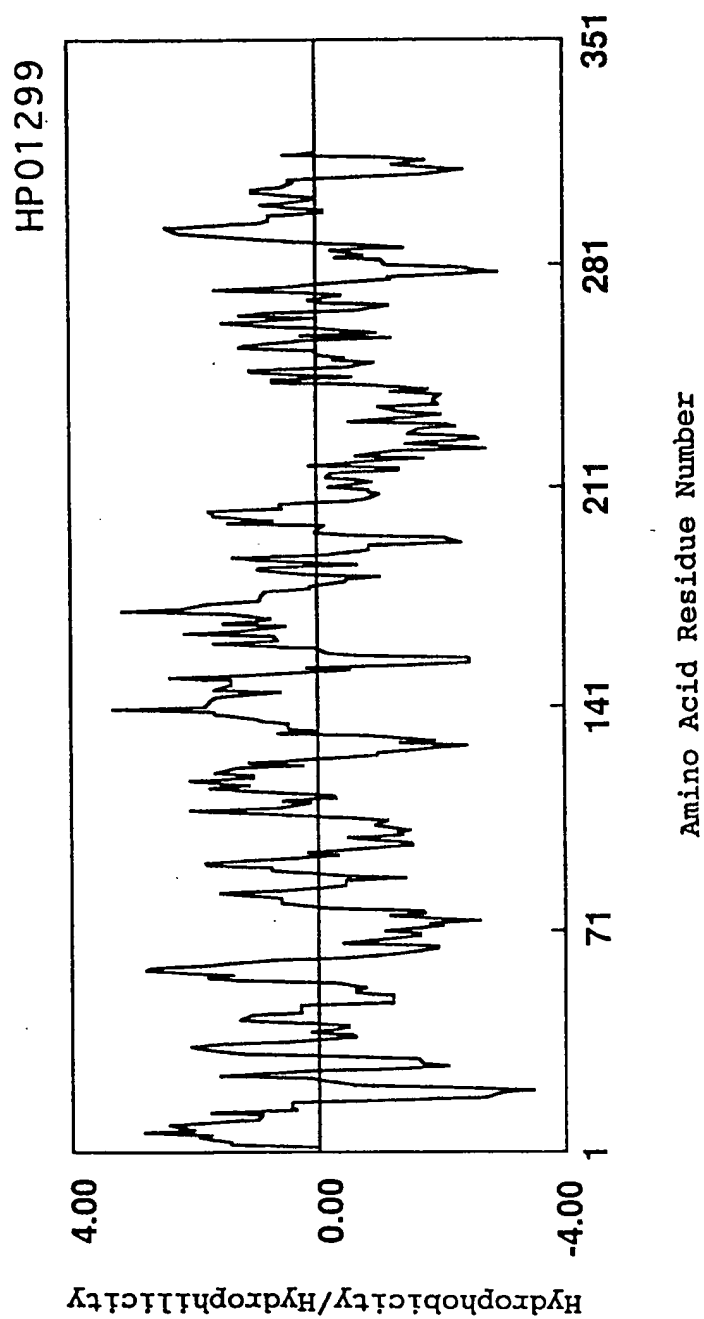


Fig.3

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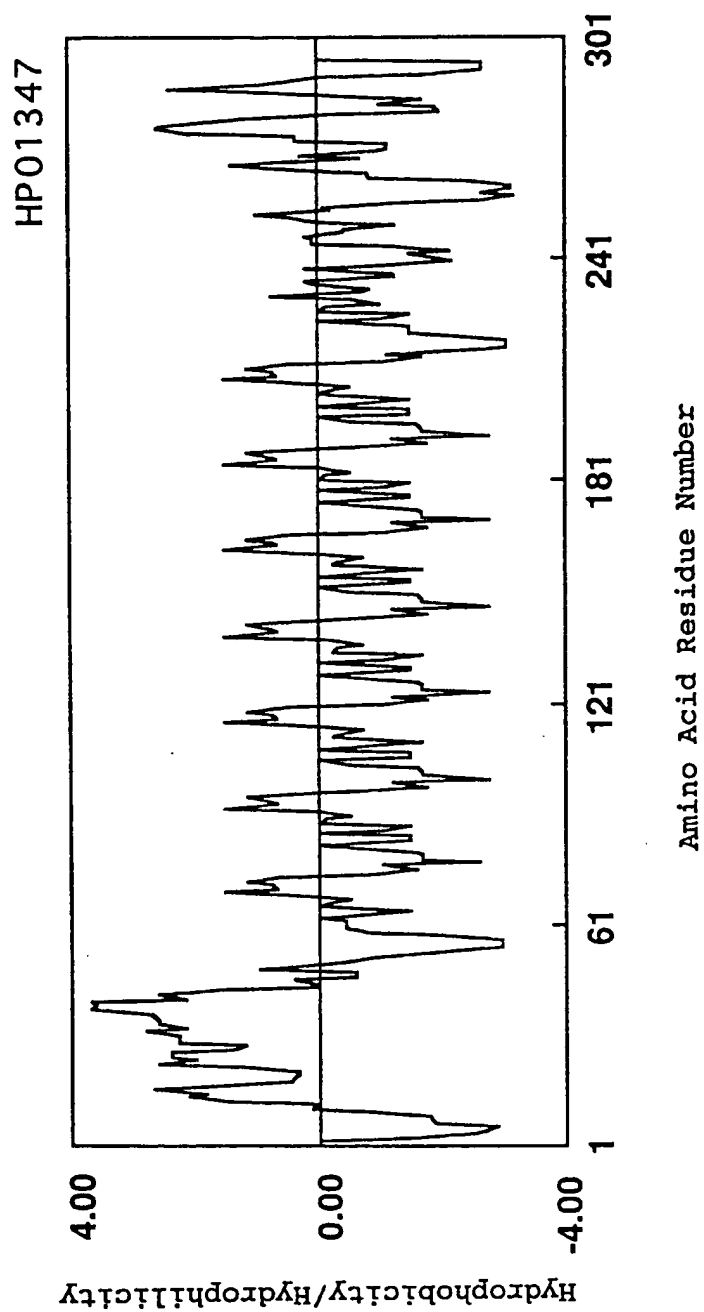


Fig.4

5/19

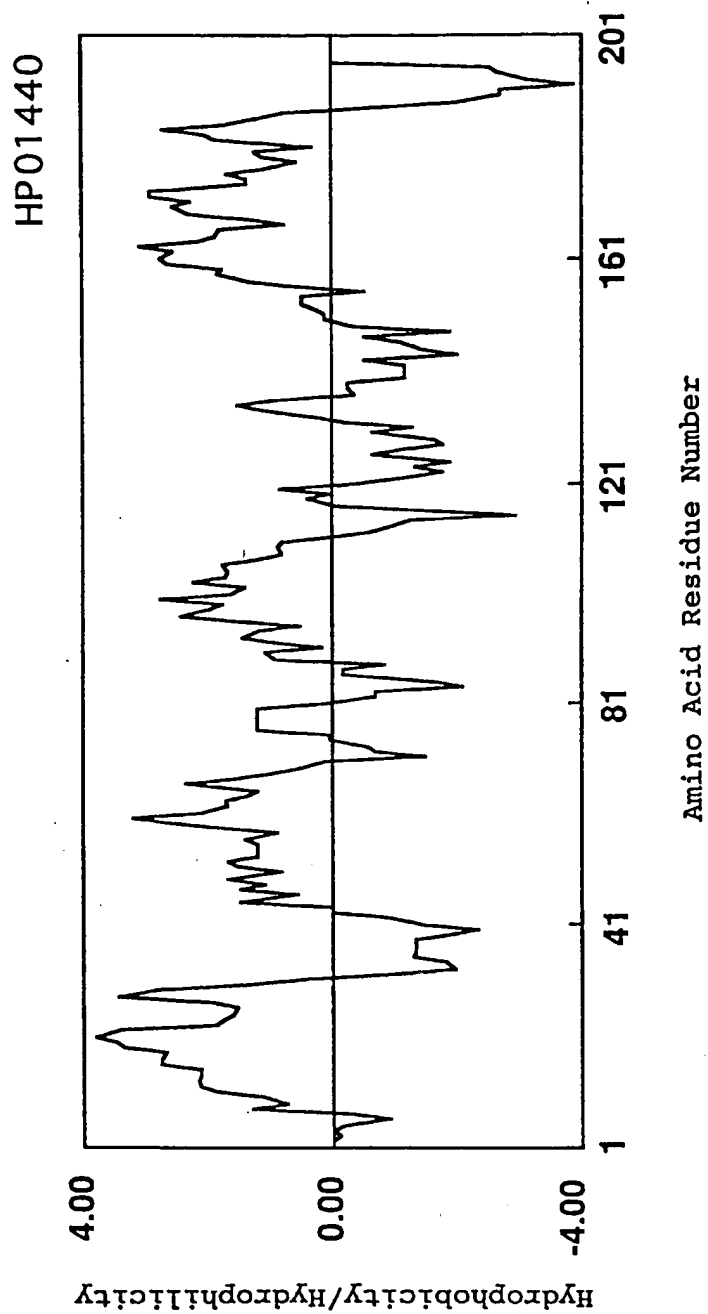


Fig.5

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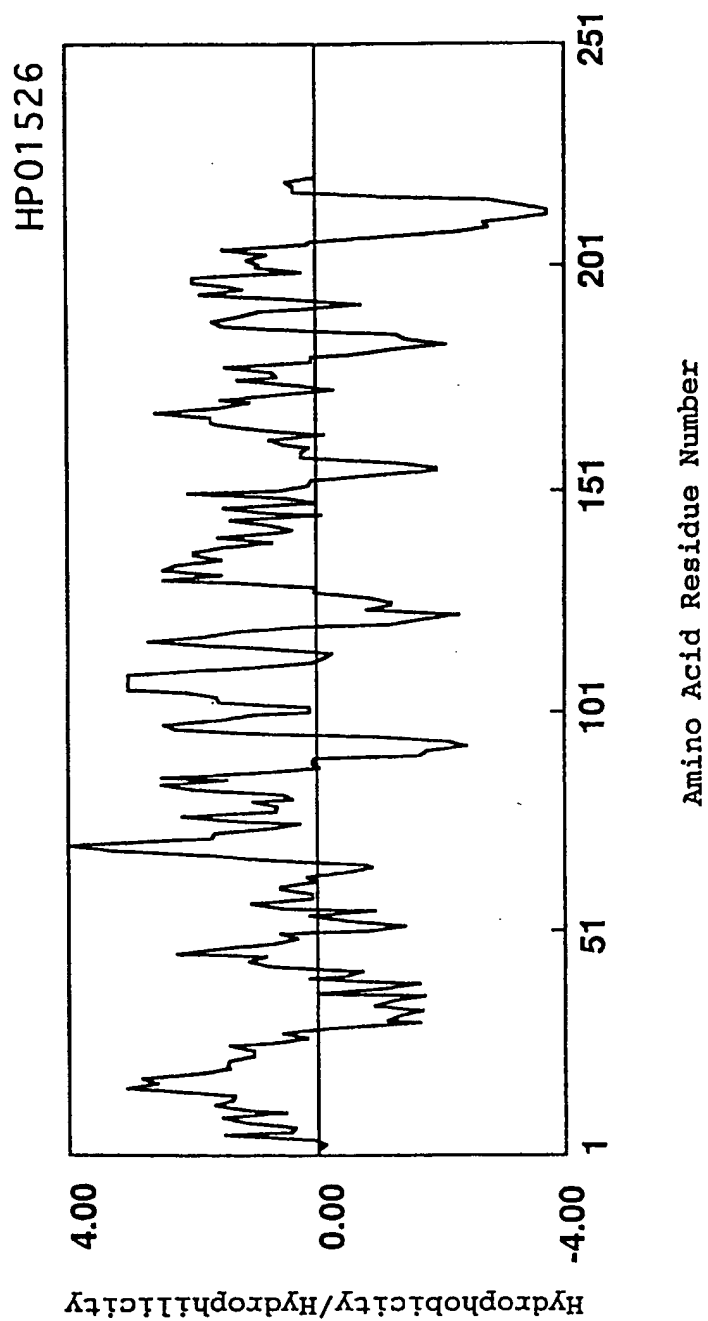


Fig.6

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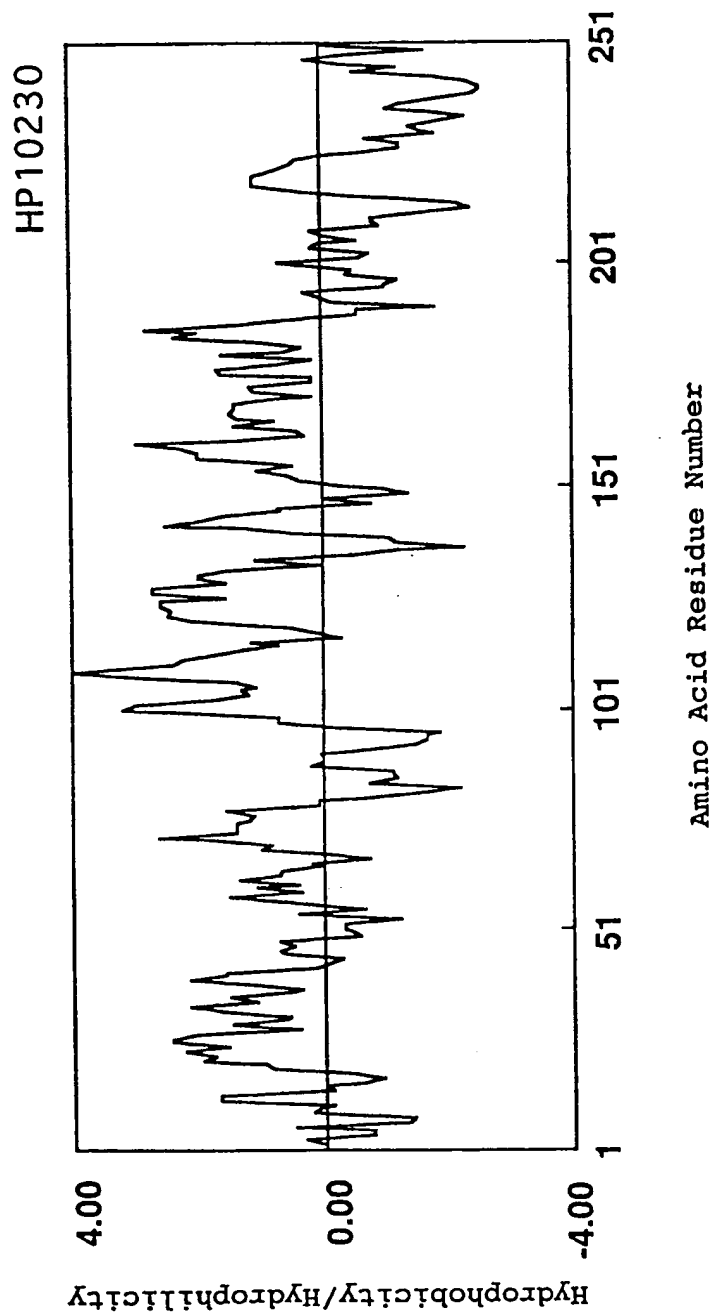


Fig.7

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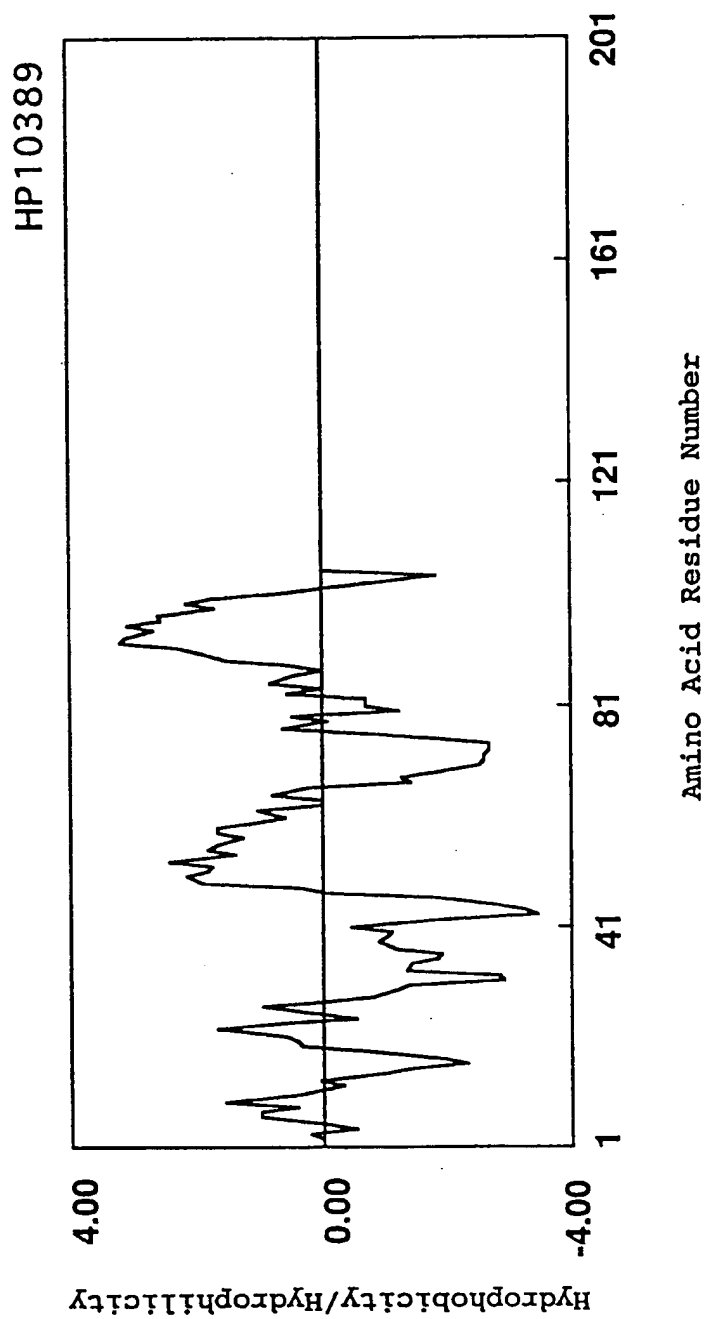


Fig.8

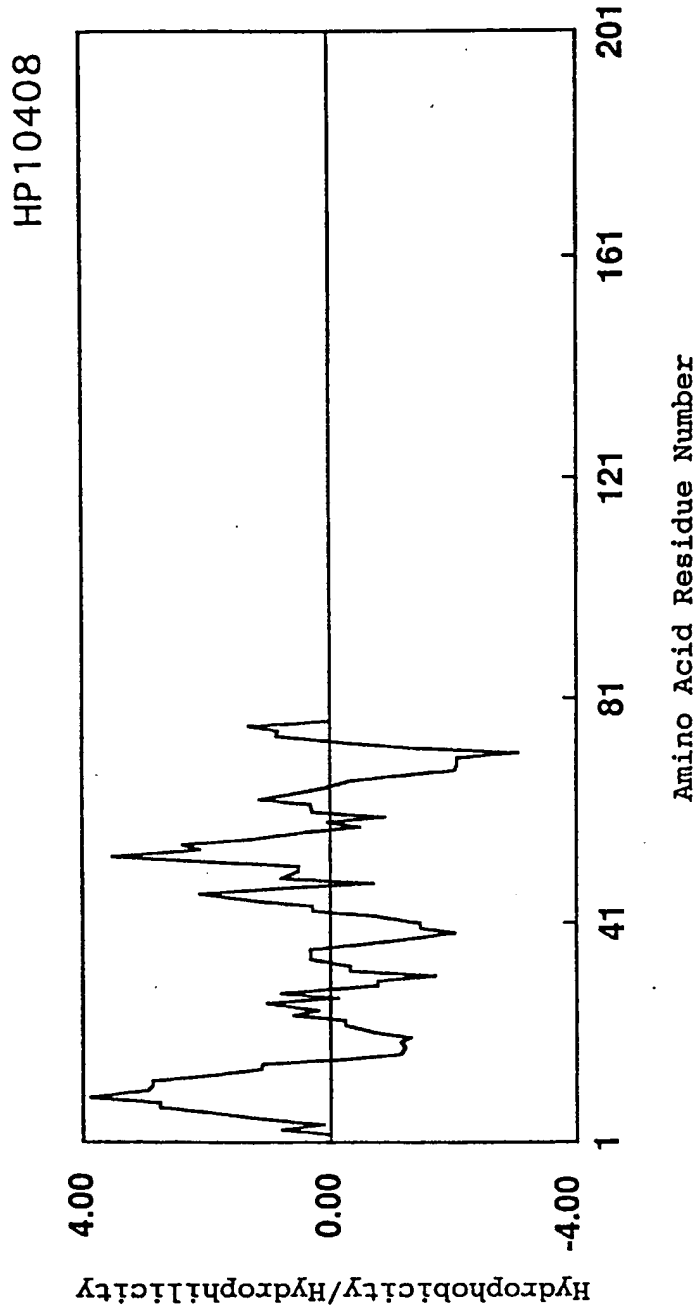


Fig.9

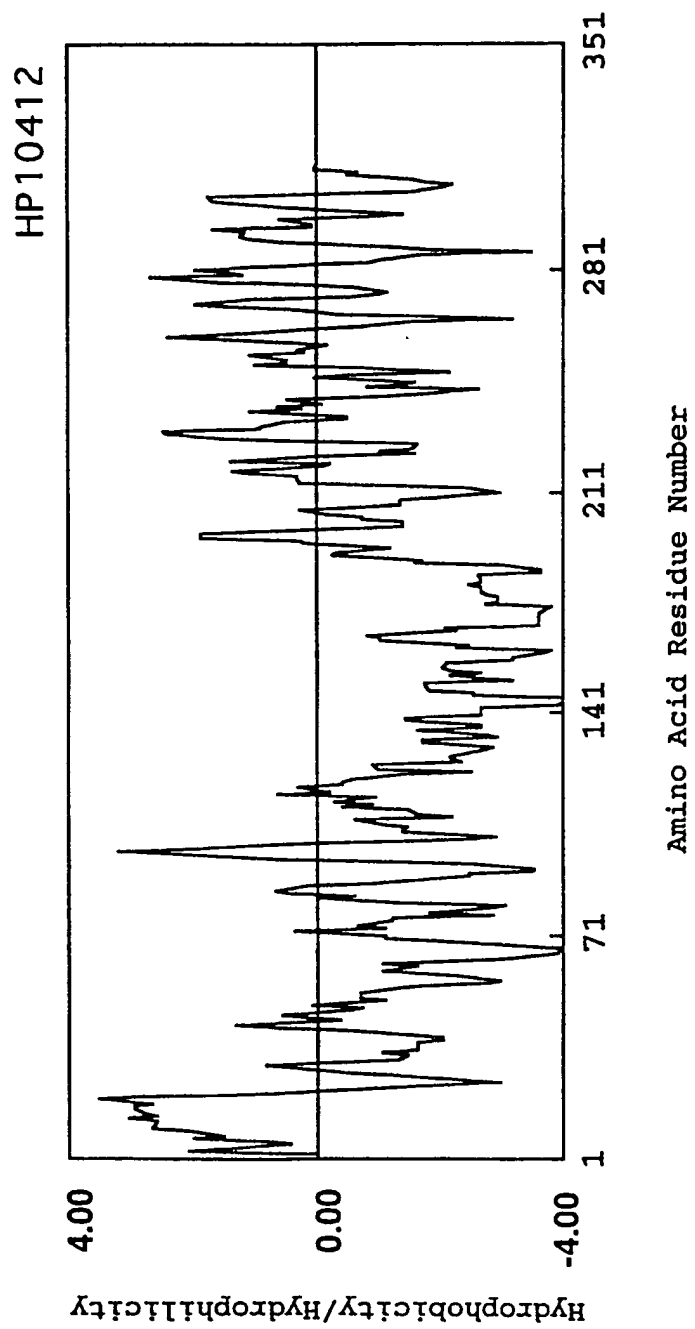


Fig.10

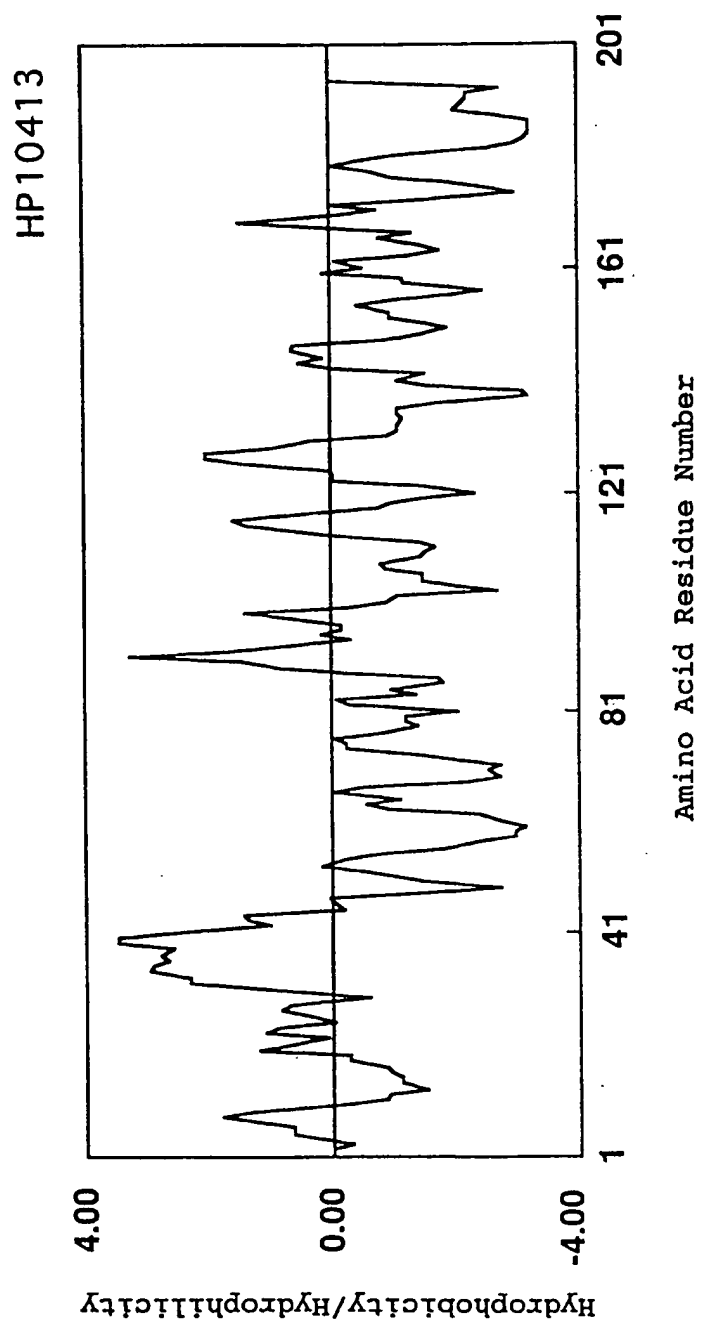


Fig.11

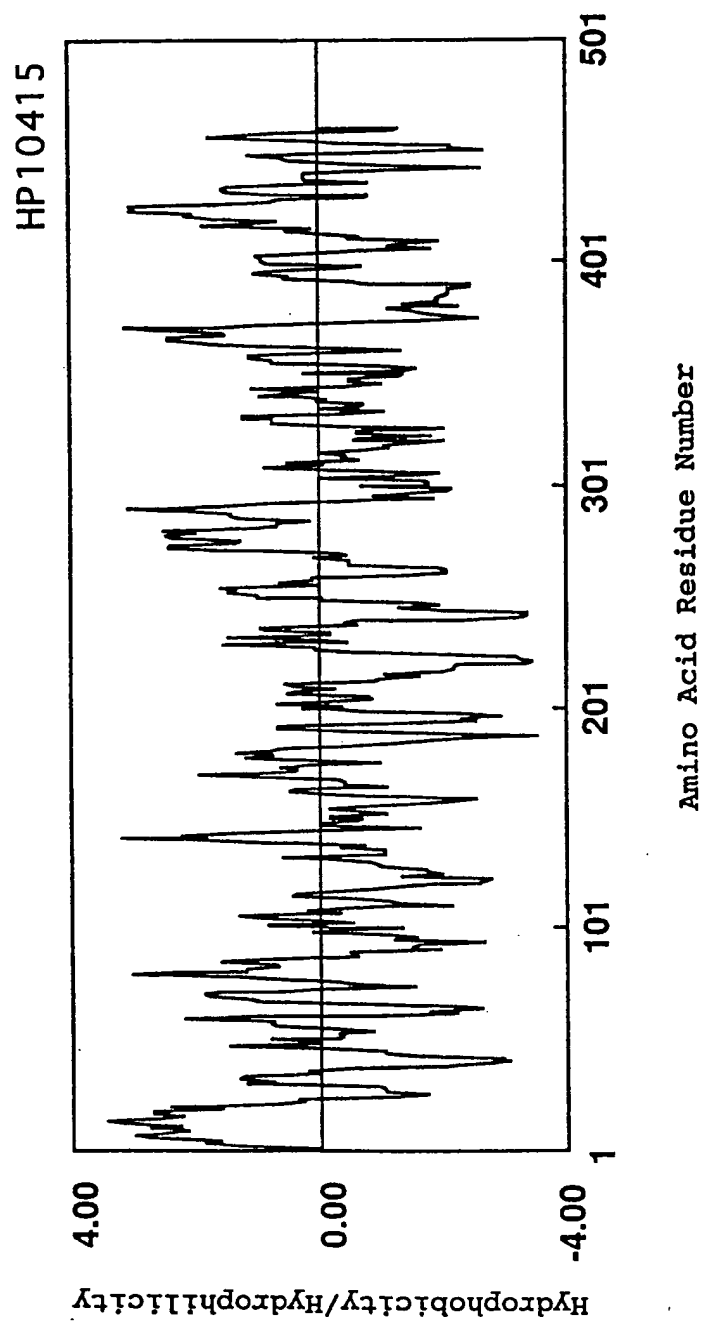


Fig.12

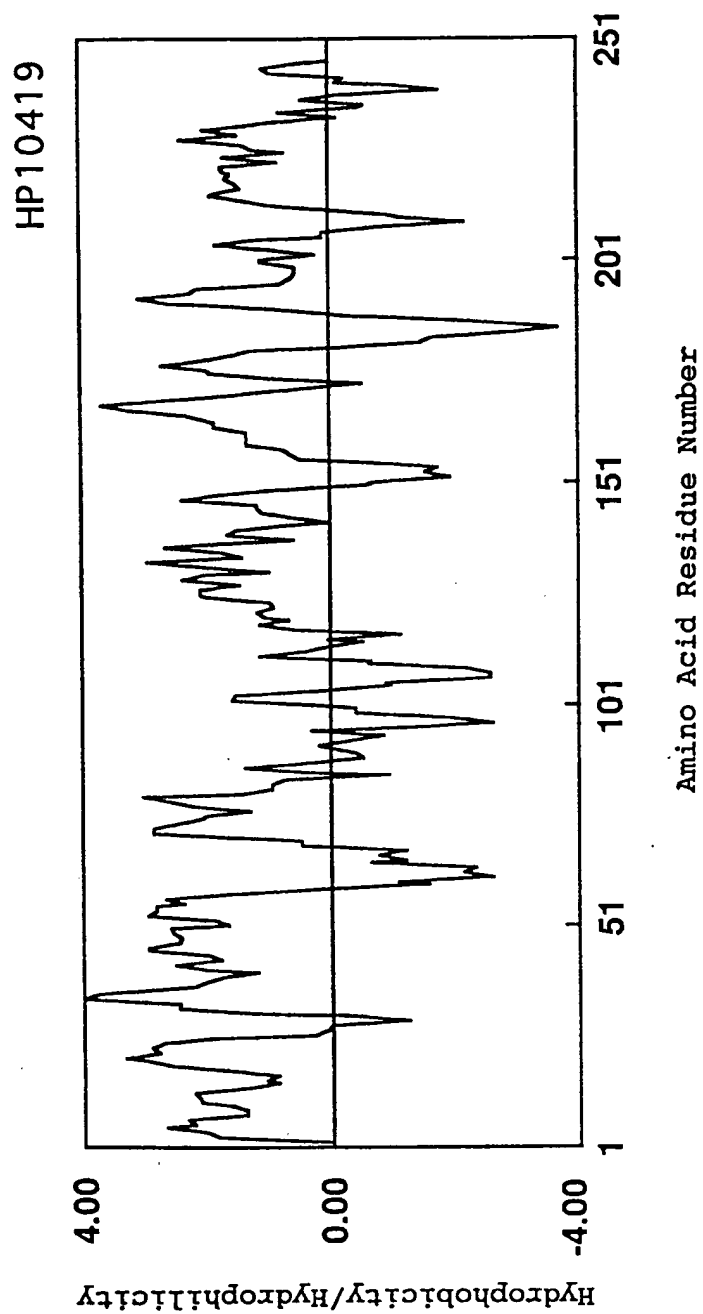


Fig.13

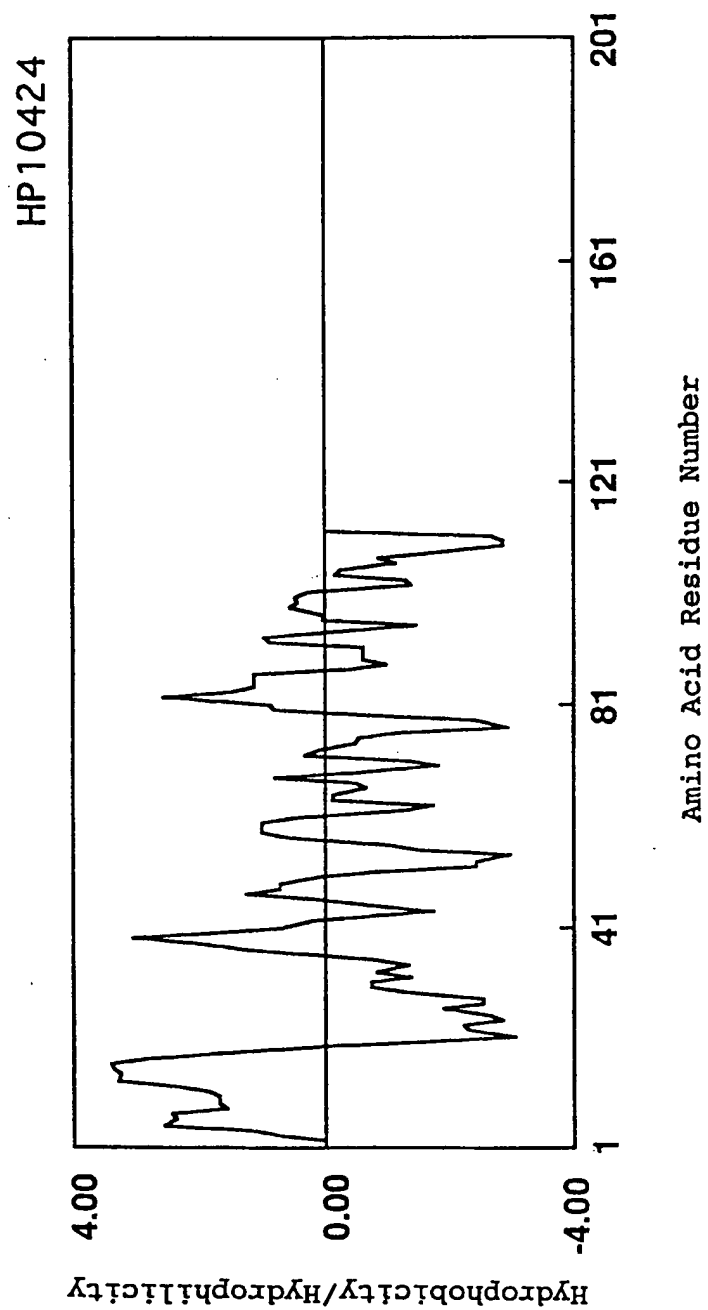


Fig.14

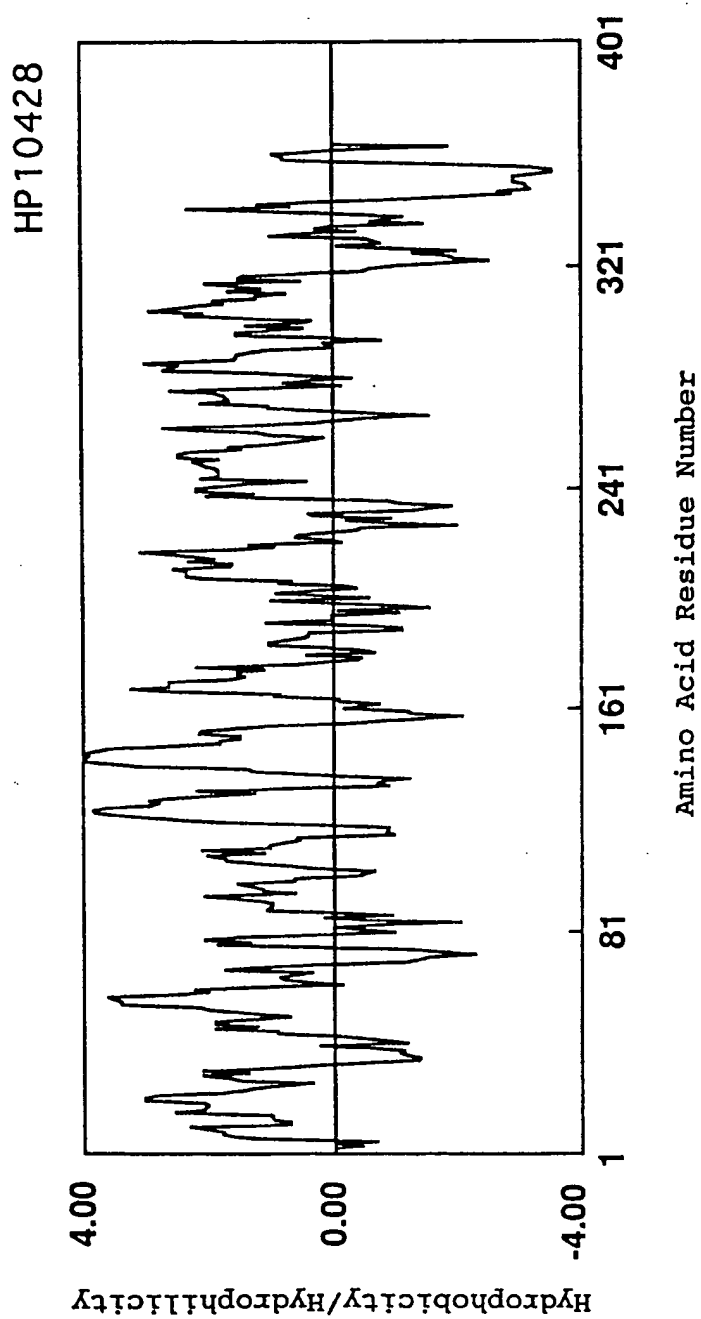


Fig.15

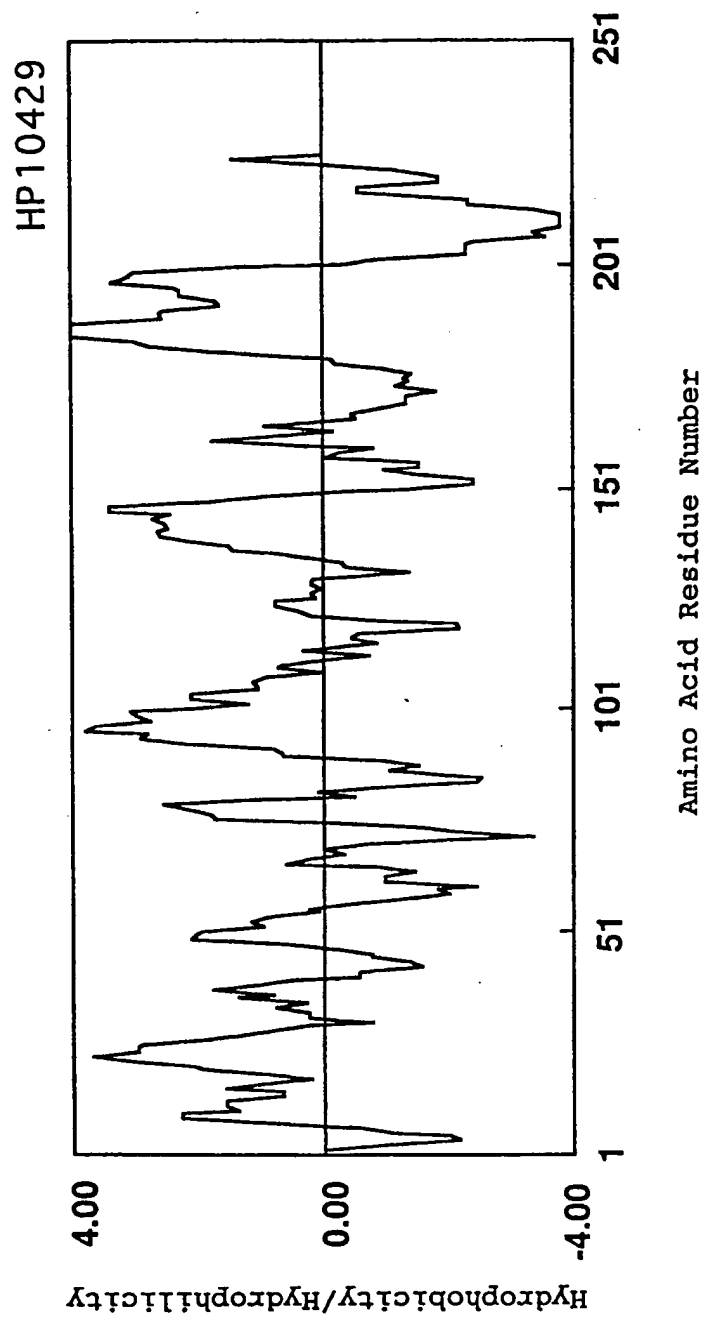


Fig.16

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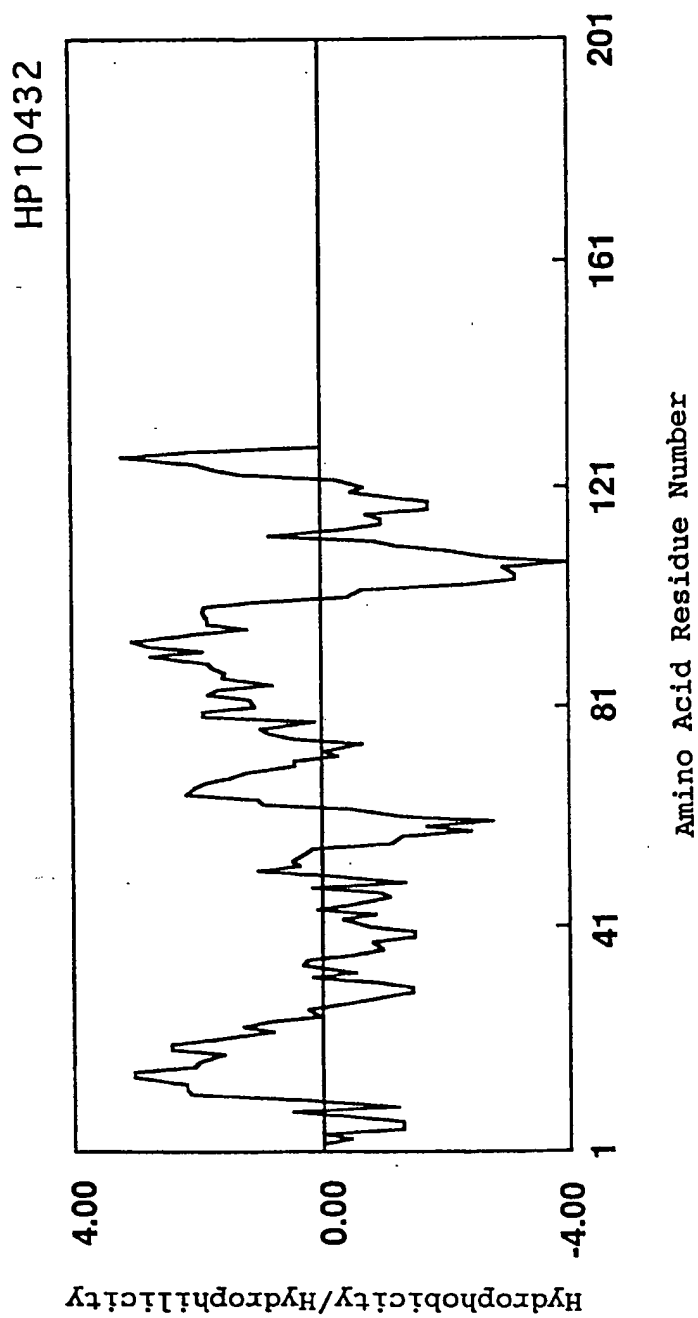


Fig.17

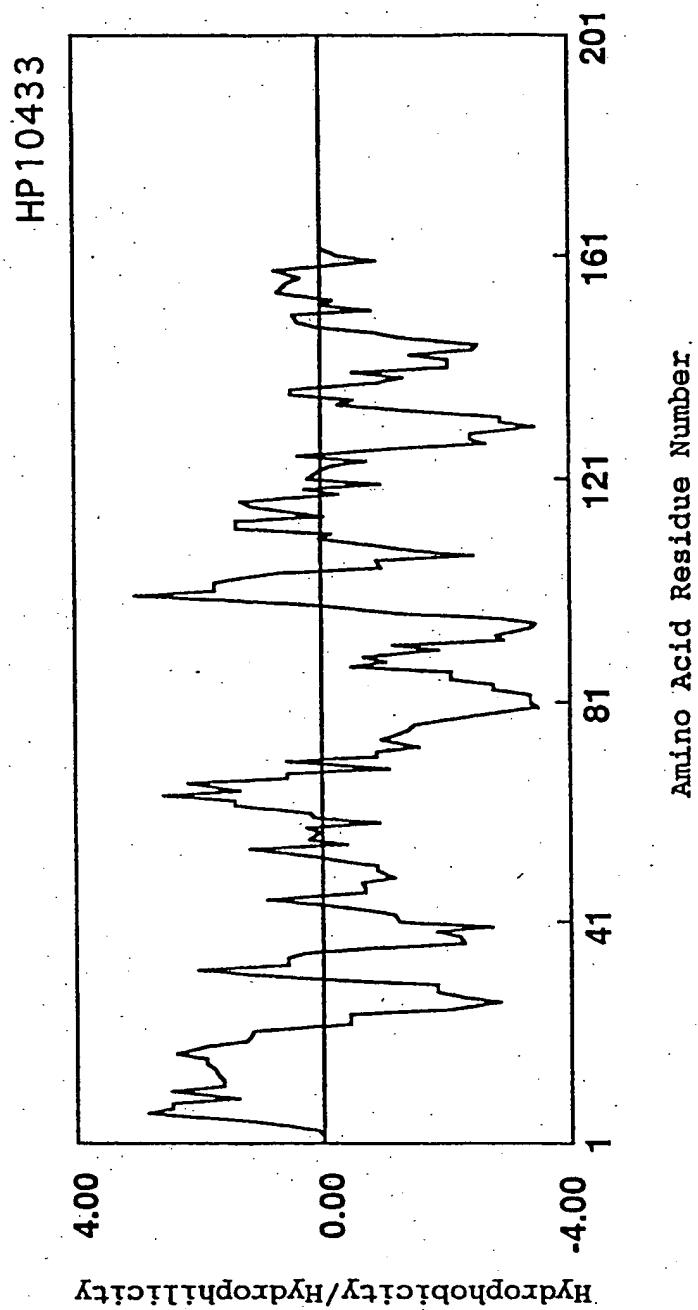


Fig.18

Fig.19

